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SEARCH REQUEST FORM

Requestor's Name: GAMBEL
Serial Number: 08/487283
Date: 7/27/97
Phone: 308-3997
Art Unit: 1806

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

SEARCH SEQ ID NO: 1

1. SEARCH INVENTORS
2. COMPLEMENT AND C5
3. (1) + (2) PRINT
4. (2) + ALPHA (w) CHAIN OR (ANTI (w) C5)
5. (4) + ANTIBOD? PRINT IF NOT TOO MUCH
6. IF (5) IS TOO MUCH, ADD (INHIBIT? OR SUPPRESS?) PRINT

STAFF USE ONLY

Date completed: 7-29-97
Searcher: AO
Terminal time:
Elapsed time:
CPU time:
Total time:
Number of Searches:
Number of Databases:

Search Site
- STIC
- x CM-1
- Pre-S

Type of Search
- N.A. Sequence
- A.A. Sequence
- Structure
- Bibliographic

Vendors
- x IG Suite
- x STN
- Dialog
- APS
- Geninfo
- SDC
- DARC/Questel
- Other

****

MPSRCH (TM)

****

Release 2.1D John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 29 07:31:34 1997; MasPar time 3.22 Seconds
188.119 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 91006 seqs, 28888923 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 25.430; Variance 35.904; scale 0.708

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	141	100.0	1676	2	C5HU	complement C5 precur	1.30e-19
2	69	48.9	1680	2	C5MS	complement C5 precur	1.21e-02
3	59	41.8	940	9	S49087	lactoferrin binding	1.09e+00
4	59	41.8	1002	12	A56678	yemanuclein-alpha -	1.09e+00
5	58	41.1	205	14	I49364	protein tyrosine pho	1.68e+00
6	58	41.1	223	14	I49365	protein tyrosine pho	1.68e+00
7	57	40.4	117	13	I68524	ribosomal protein L3	2.56e+00
8	57	40.4	264	16	S28969	N-carbamoylsarcosine	2.56e+00
9	56	39.7	537	11	B33485	spore coat protein S	3.89e+00
10	56	39.7	540	11	S21825	vicilin-like storage	3.89e+00
11	56	39.7	573	11	A53234	globulin-1S, GLB1S -	3.89e+00
12	55	39.0	775	13	A32494	transposable element	5.88e+00
13	54	38.3	148	10	E47119	spore coat peptide C	8.85e+00
14	54	38.3	224	10	G64383	riboflavin-specific	8.85e+00
15	54	38.3	562	16	S46281	P element - fruit fl	8.85e+00
16	54	38.3	818	5	S46780	hypothetical protein	8.85e+00
17	54	38.3	841	1	A30107	dipeptidyl aminopept	8.85e+00
18	54	38.3	1030	12	S57380	probable membrane pr	8.85e+00
19	53	37.6	116	4	Q4ADE5	early E4 11K protein	1.33e+01
20	53	37.6	116	4	Q4ADE2	early E4 11K protein	1.33e+01
21	53	37.6	148	7	S41772	glycine-rich RNA-bin	1.33e+01
22	53	37.6	589	7	C38128	epithelin/granulin p	1.33e+01
23	53	37.6	591	12	S43428	omega-crystallin - g	1.33e+01
24	53	37.6	669	13	I54205	galactosylceramidase	1.33e+01
25	53	37.6	1089	1	PFHUGA	platelet-derived gro	1.33e+01
26	53	37.6	1144	16	A54810	TMV resistance prote	1.33e+01
27	53	37.6	2471	14	A49128	cell-fate determinin	1.33e+01
28	52	36.9	122	11	S21823	Glb1-0 protein - mai	1.97e+01
29	52	36.9	122	11	C53234	globulin-1O, GLB1O -	1.97e+01
30	52	36.9	329	3	VMUT21	VSG expression site-	1.97e+01
31	52	36.9	354	2	DUAGO	ornithine cyclodeami	1.97e+01
32	52	36.9	354	6	S55582	methylaspartate ammo	1.97e+01
33	52	36.9	582	11	B53234	vicilin-like storage	1.97e+01
34	52	36.9	982	12	S00954	pol polyprotein - fr	1.97e+01
35	51	36.2	121	7	S48427	ribosomal protein L3	2.92e+01
36	51	36.2	121	7	S53549	ribosomal protein L3	2.92e+01
37	51	36.2	238	8	S23314	hypothetical protein	2.92e+01
38	51	36.2	250	8	S07237	hypothetical protein	2.92e+01
39	51	36.2	337	5	A35260	alcohol dehydrogenas	2.92e+01
40	51	36.2	462	5	S29004	pyruvate kinase (EC	2.92e+01
41	51	36.2	529	4	VGNVAC	major envelope glyco	2.92e+01
42	51	36.2	574	7	A37197	estrogen receptor -	2.92e+01
43	51	36.2	588	14	I53272	granulin - rat	2.92e+01
44	51	36.2	589	7	B38128	epithelin/granulin p	2.92e+01
45	51	36.2	1056	13	A53767	tracheobronchial muc	2.92e+01
46	51	36.2	1084	8	S23319	hypothetical protein	2.92e+01
47	51	36.2	1129	14	A47511	protein-tyrosine kin	2.92e+01
48	51	36.2	1132	14	JC4127	protein-tyrosine kin	2.92e+01
49	51	36.2	1291	8	S05465	retrovirus-related p	2.92e+01
50	51	36.2	1651	7	B43081	vitellogenin 6 precu	2.92e+01
51	51	36.2	1678	7	S52588	clathrin heavy chain	2.92e+01
52	50	35.5	123	7	F64093	ribosomal protein L1	4.30e+01
53	50	35.5	171	11	S56787	hypothetical protein	4.30e+01
54	50	35.5	271	4	JGEBRT	D-ribose-binding pro	4.30e+01
55	50	35.5	296	4	JGECR	D-ribose-binding pro	4.30e+01
56	50	35.5	302	3	TPCHTC	troponin T, cardiac	4.30e+01
57	50	35.5	313	13	S44474	mucin - human	4.30e+01
58	50	35.5	410	1	JN0810	benzene 1,2-dioxygen	4.30e+01
59	50	35.5	419	9	S51715	hypothetical protein	4.30e+01
60	50	35.5	547	11	S61032	hypothetical protein	4.30e+01
61	50	35.5	592	5	JQ0991	beta-fructofuranosid	4.30e+01
62	50	35.5	592	16	S61503	beta-fructofuranosid	4.30e+01
63	50	35.5	1004	12	A48821	Wnt-5 protein - frui	4.30e+01
64	50	35.5	1268	6	S33411	botulinum neurotoxin	4.30e+01
65	49	34.8	63	16	S21120	serine proteinase in	6.29e+01
66	49	34.8	72	7	S07254	variant surface glyc	6.29e+01
67	49	34.8	74	13	A45193	zinc finger protein	6.29e+01
68	49	34.8	114	10	E64467	hypothetical protein	6.29e+01
69	49	34.8	122	7	S15437	ribosomal protein L1	6.29e+01
70	49	34.8	220	16	S29195	antistasin - Hydra m	6.29e+01
71	49	34.8	222	9	S17121	phage shock protein	6.29e+01
72	49	34.8	313	11	S61990	hypothetical protein	6.29e+01
73	49	34.8	384	12	S66758	probable membrane pr	6.29e+01
74	49	34.8	424	14	S15917	developmental contro	6.29e+01
75	49	34.8	429	4	VHVUHV	nucleocapsid protein	6.29e+01
76	49	34.8	487	12	A46146	steroid receptor hom	6.29e+01
77	49	34.8	491	5	S33767	platelet-derived gro	6.29e+01
78	49	34.8	573	5	S49266	beta-fructofuranosid	6.29e+01
79	49	34.8	591	2	ISECFI	isomerase fucI (EC 5	6.29e+01
80	49	34.8	637	14	I49638	Drosophila vasa homo	6.29e+01
81	49	34.8	660	14	S24125	potassium channel pr	6.29e+01
82	49	34.8	732	9	S23001	traI protein - Esche	6.29e+01
83	49	34.8	784	13	A33633	transcription repres	6.29e+01
84	49	34.8	1088	1	PFRTGA	platelet-derived gro	6.29e+01
85	49	34.8	1323	14	I78557	NMDA receptor subuni	6.29e+01
86	49	34.8	1323	14	I58158	NMDA receptor subuni	6.29e+01
87	49	34.8	1323	7	S27224	N-methyl-D-aspartate	6.29e+01
88	49	34.8	1356	7	C45219	N-methyl-D-aspartate	6.29e+01
89	49	34.8	1451	6	B41185	alpha-2 macroglobuli	6.29e+01
90	49	34.8	1476	6	A41185	alpha-2 macroglobuli	6.29e+01
91	48	34.0	117	11	S67845	hypothetical protein	9.15e+01
92	48	34.0	229	16	S30486	hypothetical protein	9.15e+01
93	48	34.0	360	16	A49600	probable helicase -	9.15e+01
94	48	34.0	519	8	S38921	hypothetical protein	9.15e+01

95	48	34.0	845	1	JDVLVD	DNA-directed DNA pol	9.15e+01
96	48	34.0	925	5	A39216	plasma cell membrane	9.15e+01
97	48	34.0	948	8	A56602	glycoprotein B homol	9.15e+01
98	48	34.0	953	12	S55156	probable membrane pr	9.15e+01
99	48	34.0	1216	11	S46177	probable Ca2+-transp	9.15e+01
100	48	34.0	1299	12	S06119	membrane protein pat	9.15e+01

ALIGNMENTS

```
RESULT    1
ENTRY             C5HU       #type complete
TITLE             complement C5 precursor - human
CONTAINS          C5a anaphylatoxin; C5b
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                    06-Sep-1996
ACCESSIONS        A40075; A27689; A01267; A01266
REFERENCE         A40075
   #authors       Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.;
                    Wetsel, R.A.
   #journal       J. Immunol. (1991) 146:362-368
   #title         Complete cDNA sequence of human complement pro-C5. Evidence
                    of truncated transcripts derived from a single copy gene.
   #cross-references MUID:91079575
   #accession     A40075
      ##molecule_type mRNA
      ##residues      1-1676 ##label HAV
      ##cross-references GB:M57729
      ##note          518-Ser was also found
REFERENCE         A27689
   #authors       Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.;
                    Noack, D.; Tack, B.F.
   #journal       Biochemistry (1988) 27:1474-1482
   #title         Molecular analysis of human complement component C5:
                    localization of the structural gene to chromosome 9.
   #cross-references MUID:88209511
   #accession     A27689
      ##molecule_type mRNA
      ##residues      412-1676 ##label WET
      ##cross-references GB:M18879
REFERENCE         A01267
   #authors       Fernandez, H.N.; Hugli, T.E.
   #journal       J. Biol. Chem. (1978) 253:6955-6964
   #title         Primary structural analysis of the polypeptide portion of
                    human C5a anaphylatoxin. Polypeptide sequence determination
                    and assignment of the oligosaccharide attachment site in
                    C5a.
   #cross-references MUID:79005687
   #accession     A01267
      ##molecule_type protein
      ##residues      678-751 ##label FER
REFERENCE         A01266
   #authors       Lundwall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead,
                    A.S.; Woods, D.E.; Ogden, R.C.; Colten, H.R.; Tack, B.F.
   #journal       J. Biol. Chem. (1985) 260:2108-2112
   #title         Isolation and sequence analysis of a cDNA clone encoding the
                    fifth complement component.
   #cross-references MUID:85130937
   #accession     A01266
      ##molecule_type mRNA
      ##residues      412-854,
                       'SLALSPRLECNGKISGHCKLRLPGSSDSPASASQVAGITGTHHHAQPT'
                       ##label LUN
      ##cross-references GB:K02874
      ##note          the carboxyl-terminal part of the sequence in this
                       report appears to be derived from translation of an
                       ALU repeat sequence
COMMENT     Complement C5 contains two disulfide-linked chains, formed by
              removal of four basic residues. C5 convertase releases C5a
              anaphylatoxin from the amino end of the alpha chain, generating
              C5b (beta and alpha' chains).
COMMENT     Activation of C5 initiates the spontaneous assembly of the late
              complement components, C5-C9, into the membrane attack complex.
              C5b has a transient binding site for C6. The C5b-C6 complex is
              the foundation upon which the membrane attack complex is
              assembled.
COMMENT     C5a has potent spasmogenic and chemotactic activity.
GENETICS
   #gene          GDB:C5
      ##cross-references GDB:119734
   #map_position 9q33-9q33
CLASSIFICATION    #superfamily alpha-2-macroglobulin
KEYWORDS          complement alternate pathway; complement pathway; cytolysis;
                    glycoprotein; inflammatory response; membrane attack
                    complex; plasma
FEATURE
   1-18               #domain signal sequence #status predicted #label SIG\
   19-673,678-1676    #product complement C5 #status predicted #label MAT\
   19-673,752-1676    #product C5b #status predicted #label C5B\
   19-673             #product complement C5 and C5b beta chain #status
                        predicted #label C5BB\
   678-1676           #product complement C5 alpha chain #status predicted
                        #label C5A\
   678-751            #product C5a anaphylatoxin #status experimental #label
                        C5T\
   752-1676           #product C5b alpha' chain #status predicted #label C5BA\
   567-810,634-669,
   698-724,699-731,
   711-732,866-1527,
   1101-1159,
   1375-1505,
   1405-1474,
   1520-1525,
   1532-1606,
   1553-1676,
   1654-1657          #disulfide_bonds #status predicted\
   741                #binding_site carbohydrate (Asn) (covalent) #status
                        experimental\
   751-752            #cleavage_site Arg-Leu (C5 convertase) #status
                        experimental\
   911,1115,1630      #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY           #length 1676  #molecular-weight 188330  #checksum 3858

  Query Match           100.0%;  Score 141;  DB 2;  Length 1676;
  Best Local Similarity 100.0%;  Pred. No. 1.30e-19;
  Matches    21;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    872 vidhqgtksskcvrqkvegss 892
          |||||||||||||||||||||
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT    2
ENTRY             C5MS       #type complete
TITLE             complement C5 precursor - mouse
CONTAINS          C5a anaphylatoxin; C5b
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-Nov-1988 #sequence_revision 15-Oct-1994 #text_change
                    15-Oct-1994
ACCESSIONS        A35530; A27538; A40429
REFERENCE         A35530
   #authors       Wetsel, R.A.; Fleischer, D.T.; Haviland, D.L.
   #journal       J. Biol. Chem. (1990) 265:2435-2440
   #title         Deficiency of the murine fifth complement component (C5). A
                    2-base pair gene deletion in a 5'-exon.
   #cross-references MUID:90153853
   #accession     A35530
      ##molecule_type mRNA
      ##residues      1-215,'L' ##label WET
      ##cross-references GB:J05234
REFERENCE         A27538
   #authors       Wetsel, R.A.; Ogata, R.T.; Tack, B.F.
   #journal       Biochemistry (1987) 26:737-743
   #title         Primary structure of the fifth component of murine
```

```
                complement.
   #cross-references MUID:87185363
   #accession    A27538
      ##molecule_type mRNA
      ##residues       'PGL',44-1680 ##label WET2
REFERENCE        A40429
   #authors      Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Wetsel, R.A.
   #journal      J. Biol. Chem. (1991) 266:11818-11825
   #title        Structure of the murine fifth complement component (C5) gene.
                  A large, highly interrupted gene with a variant donor
                  splice site and organizational homology with the third and
                  fourth complement component genes.
   #cross-references MUID:91268053
   #accession    A40429
      ##molecule_type DNA
      ##residues      1-15 ##label HAV
      ##cross-references GB:M64852
COMMENT     Complement C5 contains two disulfide-linked chains, formed by
              removal of four basic residues. C5 convertase releases C5a
              anaphylatoxin from the amino end of the alpha chain, generating
              C5b (beta and alpha' chains).
COMMENT     Activation of C5 initiates the spontaneous assembly of the late
              complement components, C5-C9, into the membrane attack complex.
              C5b has a transient binding site for C6. The C5b-C6 complex is
              the foundation upon which the membrane attack complex is
              assembled.
COMMENT     C5a has potent spasmogenic and chemotactic activity.
GENETICS
   #map_position 2
   #introns      22/3; 86/3; 140/3; 164/3; 195/2; 223/1; 253/2; 291/3; 334/1;
                  372/3; 434/3; 502/3; 572/3; 622/3; 667/1; 691/1; 757/1;
                  787/2; 812/1; 858/3; 934/3; 955/1; 985/1; 1056/1; 1081/2;
                  1134/3; 1166/3; 1224/1; 1292/3; 1343/3; 1364/3; 1392/1;
                  1411/2; 1445/3; 1470/3; 1506/1; 1534/1; 1564/1; 1592/1;
                  1637/2
CLASSIFICATION   #superfamily alpha-2-macroglobulin
KEYWORDS         complement alternate pathway; complement pathway; cytolysis;
                  glycoprotein; inflammatory response; membrane attack
                  complex; plasma
FEATURE
   1-18              #domain signal sequence #status predicted #label SIG\
   19-674,679-1679   #product complement C5 #status predicted #label MAT\
   19-674,756-1679   #product C5b #status predicted #label C5B\
   19-674            #product complement C5 and C5b beta chain #status
                       predicted #label C5BB\
   679-1679          #product complement C5 alpha chain #status predicted
                       #label C5A\
   679-755           #product C5a anaphylatoxin #status predicted #label C5T\
   756-1679          #product C5b alpha' chain #status predicted #label C5BA\
   567-814,635-670,
   702-728,703-735,
   715-736,870-1531,
   1105-1163,
   1379-1509,
   1409-1478,
   1524-1529,
   1536-1609,
   1557-1679,
   1657-1660         #disulfide_bonds #status predicted\
   915,1119,1633     #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 1680  #molecular-weight 188876  #checksum 3888

  Query Match           48.9%;  Score 69;  DB 2;  Length 1680;
  Best Local Similarity  47.1%;  Pred. No. 1.21e-02;
  Matches     8;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db    880 htsrpsrcvfqriegss 896
          : :::|:|| |::|||
Qy      5 QGTKSSKCVRQKVEGSS 21


RESULT    3
ENTRY            S49087     #type complete
TITLE            lactoferrin binding protein - Neisseria meningitidis
ORGANISM         #formal_name Neisseria meningitidis
DATE             16-Feb-1995 #sequence_revision 12-May-1995 #text_change
                   12-May-1995
ACCESSIONS       S49087
REFERENCE        S49087
   #authors      Pettersson, A.M.; Klarenbeek, X.Y.Z.; van Deurzen, X.Y.Z.;
                   Poolman, X.Y.Z.; Tommassen, X.Y.Z.
   #submission   submitted to the EMBL Data Library, June 1994
   #description  Molecular charactarization of the structural gene for the
                   lacto-ferrin receptor of the meningococcal strain H44/76.
   #accession    S49087
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-940 ##label PET
      ##cross-references EMBL:X79838
SUMMARY          #length 940  #molecular-weight 105347  #checksum 8194

  Query Match           41.8%;  Score 59;  DB 9;  Length 940;
  Best Local Similarity  50.0%;  Pred. No. 1.09e+00;
  Matches     7;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db    592 rsrkcvprkingsn 605
          :| ||| :|::||:
Qy      8 KSSKCVRQKVEGSS 21


RESULT    4
ENTRY            A56678     #type complete
TITLE            yemanuclein-alpha - fruit fly (Drosophila melanogaster)
ORGANISM         #formal_name Drosophila melanogaster
DATE             08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                   11-Aug-1995
ACCESSIONS       A56678; S22146
REFERENCE        A56678
   #authors      Ait-Ahmed, O.; Bellon, B.; Capri, M.; Joblet, C.;
                   Thomas-Delaage, M.
   #journal      Mech. Dev. (1992) 37:69-80
   #title        The yemanuclein-alpha: a new Drosophila DNA binding protein
                   specific for the oocyte nucleus.
   #accession    A56678
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-1002 ##label AIE
      ##cross-references GB:X63503
GENETICS
   #introns      80/3; 154/3; 428/1 477/2; 557/2
KEYWORDS         DNA binding; oocyte
SUMMARY          #length 1002  #molecular-weight 109310  #checksum 4278

  Query Match           41.8%;  Score 59;  DB 12;  Length 1002;
  Best Local Similarity  50.0%;  Pred. No. 1.09e+00;
  Matches     6;  Conservative    5;  Mismatches   1;  Indels   0;  Gaps   0;

Db     47 tktakcirikld 58
          ||::||:| |::
Qy      7 TKSSKCVRQKVE 18


RESULT    5
ENTRY            I49364     #type complete
TITLE            protein tyrosine phosphatase - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                   02-Jul-1996
ACCESSIONS       I49364
REFERENCE        I49364
   #authors      Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
   #journal      J. Biol. Chem. (1995) 270:26782-26785
   #title        A single mutation converts a novel-phosphotyrosine binding
                   domain into a dual-specificity phosphatase.
   #accession    I49364
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     ##status        preliminary; translated from GB/EMBL/DDBJ
     ##molecule_type mRNA
     ##residues      1-205 ##label RES
     ##cross-references EMBL:U34973; NID:g1063624; CDS_PID:g1063625
SUMMARY          #length 205  #molecular-weight 23683  #checksum 2745

  Query Match           41.1%;  Score 58;  DB 14;  Length 205;
  Best Local Similarity  25.0%;  Pred. No. 1.68e+00;
  Matches     5;  Conservative    9;  Mismatches   6;  Indels   0;  Gaps   0;

Db     51 ilqkhgithiicirqniean 70
          ::: :|     |:||::|::
Qy      1 VIDHQGTKSSKCVRQKVEGS 20


RESULT    6
ENTRY            I49365     #type complete
TITLE            protein tyrosine phosphatase - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                   02-Jul-1996
ACCESSIONS       I49365
REFERENCE        I49364
   #authors      Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
   #journal      J. Biol. Chem. (1995) 270:26782-26785
   #title        A single mutation converts a novel-phosphotyrosine binding
                   domain into a dual-specificity phosphatase.
   #accession    I49365
     ##status        preliminary; translated from GB/EMBL/DDBJ
     ##molecule_type mRNA
     ##residues      1-223 ##label RES
     ##cross-references EMBL:U34973; NID:g1063624; CDS_PID:g1063626
GENETICS
   #introns      168/3
SUMMARY          #length 223  #molecular-weight 25416  #checksum 359

  Query Match           41.1%;  Score 58;  DB 14;  Length 223;
  Best Local Similarity  25.0%;  Pred. No. 1.68e+00;
  Matches     5;  Conservative    9;  Mismatches   6;  Indels   0;  Gaps   0;

Db     51 ilqkhgithiicirqniean 70
          ::: :|     |:||::|::
Qy      1 VIDHQGTKSSKCVRQKVEGS 20


RESULT    7
ENTRY            I68524     #type complete
TITLE            ribosomal protein L34 - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             24-May-1996 #sequence_revision 24-May-1996 #text_change
                   24-May-1996
ACCESSIONS       I68524
REFERENCE        I54209
   #authors      Rommens, J.M.; Durocher, F.; McArthur, J.; Tonin, P.;
                   Leblanc, J.
   #journal      Genomics (1995) 28:530-542
   #title        Generation of a transcription map at the HSD17B locus
                   centromeric to BRCA1 at 17q21.
   #accession    I68524
     ##status        preliminary; translated from GB/EMBL/DDBJ
     ##molecule_type mRNA
     ##residues      1-117 ##label RES
     ##cross-references GB:L38941; NID:g1008855; CDS_PID:g1008856
SUMMARY          #length 117  #molecular-weight 13305  #checksum 4392

  Query Match           40.4%;  Score 57;  DB 13;  Length 117;
  Best Local Similarity  41.7%;  Pred. No. 2.56e+00;
  Matches     5;  Conservative    6;  Mismatches   1;  Indels   0;  Gaps   0;

Db     80 gsmcakcvrdri 91
          |:: :||||:::
Qy      6 GTKSSKCVRQKV 17


RESULT    8
ENTRY            S28969     #type complete
TITLE            N-carbamoylsarcosine amidohydrolase (EC 3.5.1.59) -
                   Arthrobacter sp.
ORGANISM         #formal_name Arthrobacter sp.
DATE             22-Nov-1993 #sequence_revision 22-Nov-1993 #text_change
                   22-Nov-1993
ACCESSIONS       S28969
REFERENCE        S28969
   #authors      Romao, M.J.; Turk, D.; Gomis-Rueth, F.X.; Huber, R.;
                   Schumacher, G.; Moellering, H.; Ruessmann, L.
   #journal      J. Mol. Biol. (1992) 226:1111-1130
   #title        Crystal structure analysis, refinement and enzymatic reaction
                   mechanism of N-carbamoylsarcosine amidohydrolase from
                   Arthrobacter sp. at 2.0 A resolution.
   #accession    S28969
     ##status        preliminary
     ##residues      1-264 ##label ROM
SUMMARY          #length 264  #molecular-weight 29057  #checksum 6729

  Query Match           40.4%;  Score 57;  DB 16;  Length 264;
  Best Local Similarity  40.0%;  Pred. No. 2.56e+00;
  Matches     6;  Conservative    5;  Mismatches   4;  Indels   0;  Gaps   0;

Db    171 gataagcvrhtveda 185
          |: :: |||: || :
Qy      6 GTKSSKCVRQKVEGS 20


RESULT    9
ENTRY            B33485     #type complete
TITLE            spore coat protein SP70 - slime mold (Dictyostelium
                   discoideum)
ORGANISM         #formal_name Dictyostelium discoideum
DATE             09-Mar-1990 #sequence_revision 11-Sep-1992 #text_change
                   30-Sep-1993
ACCESSIONS       B33485
REFERENCE        A33485
   #authors      Fosnaugh, K.L.; Loomis, W.F.
   #journal      Mol. Cell. Biol. (1989) 9:5215-5218
   #title        Spore coat genes SP60 and SP70 of Dictyostelium discoideum.
   #cross-references MUID:90097939
   #accession    B33485
     ##status        preliminary
     ##molecule_type DNA; mRNA
     ##residues      1-537 ##label FOS
     ##cross-references GB:M26238
     ##note          the authors translated the codon AAT for residue 281 as
                      Asp
CLASSIFICATION   #superfamily LDL receptor ligand-binding repeat homology
SUMMARY          #length 537  #molecular-weight 56650  #checksum 2250

  Query Match           39.7%;  Score 56;  DB 11;  Length 537;
  Best Local Similarity  54.5%;  Pred. No. 3.89e+00;
  Matches     6;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;

Db    291 kngecirdkve 301
          |:: |:|:|||
Qy      8 KSSKCVRQKVE 18


RESULT   10
ENTRY            S21825     #type complete
TITLE            vicilin-like storage protein Glb1-S, embryo - maize
ORGANISM         #formal_name Zea mays #common_name maize
DATE             20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                   20-Feb-1995
ACCESSIONS       S21825
REFERENCE        S21823
   #authors      Kriz, A.L.
   #submission   submitted to the EMBL Data Library, April 1991
   #accession    S21825
```

```
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-540 ##label KRI
      ##cross-references EMBL:X59084
GENETICS
   #gene          Glb1-S
   #introns       170/1; 195/2; 222/2; 319/2
SUMMARY           #length 540  #molecular-weight 60239  #checksum 1419

  Query Match           39.7%;  Score 56;  DB 11;  Length 540;
  Best Local Similarity  58.3%;  Pred. No. 3.89e+00;
  Matches     7;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;

Db      32 hgghksgrcvrr 43
           | |  ||::|||:
Qy       4 HQGTKSSKCVRQ 15


RESULT   11
ENTRY             A53234     #type complete
TITLE             globulin-1S, GLB1S - maize
ORGANISM          #formal_name Zea mays #common_name maize
DATE              02-May-1994 #sequence_revision 18-Nov-1994 #text_change
                    05-Apr-1995
ACCESSIONS        A53234
REFERENCE         A53234
   #authors       Belanger, F.C.; Kriz, A.L.
   #journal       Genetics (1991) 129:863-872
   #title         Molecular basis for allelic polymorphism of the maize
                    Globulin-1 gene.
   #cross-references MUID:92090707
   #accession     A53234
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-573 ##label BEL
      ##cross-references NCBIN:71280; NCBIP:71284
      ##experimental_source inbred line Va 26
      ##note          sequence extracted from NCBI backbone
SUMMARY           #length 573  #molecular-weight 65075  #checksum 3569

  Query Match           39.7%;  Score 56;  DB 11;  Length 573;
  Best Local Similarity  58.3%;  Pred. No. 3.89e+00;
  Matches     7;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;

Db      32 hgghksgrcvrr 43
           | |  ||::|||:
Qy       4 HQGTKSSKCVRQ 15


RESULT   12
ENTRY             A32494     #type complete
TITLE             transposable element Txlc protein 1 - African clawed frog
ORGANISM          #formal_name Xenopus laevis #common_name African clawed frog
DATE              12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change
                    31-Dec-1993
ACCESSIONS        A32494
REFERENCE         A32494
   #authors       Garrett, J.E.; Knutzon, D.S.; Carroll, D.
   #journal       Mol. Cell. Biol. (1989) 9:3018-3027
   #title         Composite transposable elements in the Xenopus laevis genome.
   #cross-references MUID:89384562
   #accession     A32494
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-775 ##label GAR
      ##cross-references GB:M26915
      ##note          the authors translated the codon ATT for residue as Gln,
                       and AAG for residue 288 as Leu
SUMMARY           #length 775  #molecular-weight 82355  #checksum 6734

  Query Match           39.0%;  Score 55;  DB 13;  Length 775;
  Best Local Similarity  46.7%;  Pred. No. 5.88e+00;
  Matches     7;  Conservative    5;  Mismatches   3;  Indels   0;  Gaps   0;

Db     617 sntskcvssevegtp 631
           :::||||   |||::
Qy       7 TKSSKCVRQKVEGSS 21


RESULT   13
ENTRY             E47119     #type complete
TITLE             spore coat peptide CotZ - Bacillus subtilis
ORGANISM          #formal_name Bacillus subtilis
DATE              21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
                    18-Nov-1994
ACCESSIONS        E47119
REFERENCE         A47119
   #authors       Zhang, J.; Fitz-James, P.C.; Aronson, A.I.
   #journal       J. Bacteriol. (1993) 175:3757-3766
   #title         Cloning and characterization of a cluster of genes encoding
                    polypeptides present in the insoluble fraction of the spore
                    coat of Bacillus subtilis.
   #cross-references MUID:93285989
   #accession     E47119
      ##status        preliminary
      ##molecule_type nucleic acid
      ##residues      1-148 ##label ZHA
      ##cross-references NCBIN:133538; NCBIP:133548
      ##note          sequence extracted from NCBI backbone
SUMMARY           #length 148  #molecular-weight 16534  #checksum 4681

  Query Match           38.3%;  Score 54;  DB 10;  Length 148;
  Best Local Similarity  63.6%;  Pred. No. 8.85e+00;
  Matches     7;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db       4 ktsscvreave 14
           |:| |||: ||
Qy       8 KSSKCVRQKVE 18


RESULT   14
ENTRY             G64383     #type complete
TITLE             riboflavin-specific deaminase (EC 3.5.4.-) - Methanococcus
                    jannaschii
ORGANISM          #formal_name Methanococcus jannaschii
DATE              13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
                    13-Sep-1996
ACCESSIONS        G64383
REFERENCE         A64300
   #authors       Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
                    R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton,
                    R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
                    Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
                    Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
                    Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann,
                    J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson,
                    J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
                    K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk,
                    H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
   #journal       Science (1996) 273:1058-1073
   #title         Complete genome sequence of the methanogenic archaeon,
                    Methanococcus jannaschii.
   #accession     G64383
      ##status        preliminary; nucleic acid sequence not shown;
                        translation not shown
      ##molecule_type DNA
      ##residues      1-224 ##label BUL
      ##cross-references GB:L77117; TIGR:MJ0671; CDS_PID:g1510756
GENETICS
   #map_position REV597638-596964
   #start_codon  TTG
KEYWORDS          hydrolase
SUMMARY           #length 224  #molecular-weight 25037  #checksum 2215

  Query Match           38.3%;  Score 54;  DB 10;  Length 224;
  Best Local Similarity  33.3%;  Pred. No. 8.85e+00;
```

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  Matches     6;  Conservative     4;  Mismatches   8;  Indels   0;  Gaps   0;

Db    118 iledmgvevvkcgrgkvd 135
          :::  |    || | ||:
Qy      1 VIDHQGTKSSKCVRQKVE 18


RESULT   15
ENTRY            S46281     #type complete
TITLE            P element - fruit fly (Drosophila ananassae)
ORGANISM         #formal_name Drosophila bifasciata
DATE             01-Feb-1995 #sequence_revision 01-Feb-1995 #text_change
                   01-Feb-1995
ACCESSIONS       S46281
REFERENCE        S46281
   #authors      Hagemann, S.; Miller, W.J.; Pinsker, W.
   #journal      Mol. Gen. Genet. (1994) 244:168-175
   #title        Two distinct P element subfamilies in the genome of
                   Drosophila bifasciata.
   #accession    S46281
      ##status        preliminary
      ##residues      1-562 ##label HAG
SUMMARY          #length 562  #molecular-weight 64682  #checksum 782

  Query Match           38.3%;  Score 54;  DB 16;  Length 562;
  Best Local Similarity  41.2%;  Pred. No. 8.85e+00;
  Matches     7;  Conservative     5;  Mismatches   5;  Indels   0;  Gaps   0;

Db     97 vinhstsmeiktlrqki 113
          ||:|  ::  | :|||:
Qy      1 VIDHQGTKSSKCVRQKV 17


RESULT   16
ENTRY            S46780     #type complete
TITLE            hypothetical protein YHR028c - yeast (Saccharomyces
                   cerevisiae)
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                   03-May-1996
ACCESSIONS       S46780
REFERENCE        S46772
   #authors      Du, Z.
   #submission   submitted to the EMBL Data Library, June 1994
   #description  The sequence of S. cerevisiae cosmid 8082.
   #accession    S46780
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-818 ##label DUZ
      ##cross-references EMBL:U10399
GENETICS
   #map_position 8R
CLASSIFICATION   #superfamily dipeptidyl-peptidase IV
SUMMARY          #length 818  #molecular-weight 93404  #checksum 2391

  Query Match           38.3%;  Score 54;  DB 5;  Length 818;
  Best Local Similarity  33.3%;  Pred. No. 8.85e+00;
  Matches     7;  Conservative     7;  Mismatches   7;  Indels   0;  Gaps   0;

Db    511 ivdfhsrkaekcdkgnvlgks 531
          ::| :: |: || : :| | |
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   17
ENTRY            A30107     #type complete
TITLE            dipeptidyl aminopeptidase B (EC 3.4.14.-) - yeast
                   (Saccharomyces cerevisiae)
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             07-Jun-1990 #sequence_revision 08-Mar-1996 #text_change
                   25-Oct-1996
ACCESSIONS       A30107
REFERENCE        A30107
   #authors      Roberts, C.J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.
   #journal      J. Cell Biol. (1989) 108:1363-1373
   #title        Structure, biosynthesis, and localization of dipeptidyl
                   aminopeptidase B, an integral membrane glycoprotein of the
                   yeast vacuole.
   #cross-references MUID:89174971
   #accession    A30107
      ##molecule_type DNA
      ##residues      1-841 ##label ROB
      ##cross-references EMBL:X15484
      ##note          the authors translated the codon ACC for residue 571 as
                       Asn
GENETICS
   #gene         LISTA:DAP2; STE13
   #map_position 15R
CLASSIFICATION   #superfamily dipeptidyl-peptidase IV
KEYWORDS         dipeptidylpeptide hydrolase; glycoprotein; transmembrane
                   protein
FEATURE
   30-45              #domain transmembrane #status predicted #label TMM\
   63,79,110,139,391,
   420                #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY          #length 841  #molecular-weight 96416  #checksum 1272

  Query Match           38.3%;  Score 54;  DB 1;  Length 841;
  Best Local Similarity  33.3%;  Pred. No. 8.85e+00;
  Matches     7;  Conservative     7;  Mismatches   7;  Indels   0;  Gaps   0;

Db    510 ivdfhsrkaekcdkgnvlgks 530
          ::| :: |: || : :| | |
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   18
ENTRY            S57380     #type complete
TITLE            probable membrane protein YOL089c - yeast (Saccharomyces
                   cerevisiae)
ALTERNATE_NAMES  hypothetical protein O0938
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
                   02-Aug-1996
ACCESSIONS       S57380; S66783; S50416
REFERENCE        S57374
   #authors      Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer,
                   M.
   #journal      Yeast (1995) 11:975-986
   #title        A 29.425 kb segment on the left arm of yeast chromosome XV
                   contains more than twice as many unknown as known open
                   reading frames.
   #accession    S57380
      ##status        nucleic acid sequence not shown
      ##molecule_type DNA
      ##residues      1-1030 ##label ZUM
      ##cross-references EMBL:X83121
REFERENCE        S66775
   #authors      Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer,
                   M.
   #submission   submitted to the Protein Sequence Database, July 1996
   #accession    S66783
      ##molecule_type DNA
      ##residues      1-1030 ##label ZUW
      ##cross-references EMBL:Z74831
      ##experimental_source strain S288C
GENETICS
   #map_position 15L
CLASSIFICATION   #superfamily GAL4 zinc binuclear cluster homology
KEYWORDS         transmembrane protein
FEATURE
   131-171            #domain GAL4 zinc binuclear cluster homology #label
                        GAL4\
   762-778            #domain transmembrane #status predicted #label TMM
SUMMARY          #length 1030  #molecular-weight 117925  #checksum 6585
```

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  Query Match           38.3%;  Score 54;  DB 12;  Length 1030;
  Best Local Similarity  38.5%;  Pred. No. 8.85e+00;
  Matches     5;  Conservative    5;  Mismatches   3;  Indels   0;  Gaps   0;

Db    149 vdqqtkkcsncik 161
          :|:|  | |:|::
Qy      2 IDHQGTKSSKCVR 14


RESULT   19
ENTRY            Q4ADE5     #type complete
TITLE            early E4 11K protein - human adenovirus 5
ORGANISM         #formal_name Mastadenovirus h5 #common_name human adenovirus
                   5
   #note         host Homo sapiens (man)
DATE             31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
                   04-Mar-1994
ACCESSIONS       B03807; A03807
REFERENCE        A92890
   #authors      Sarnow, P.; Hearing, P.; Anderson, C.W.; Reich, N.; Levine,
                   A.J.
   #journal      J. Mol. Biol. (1982) 162:565-583
   #title        Identification and characterization of an immunologically
                   conserved adenovirus early region 11,000 M-r protein and
                   its association with the nuclear matrix.
   #cross-references MUID:83164198
   #accession    B03807
      ##molecule_type DNA
      ##residues      1-116 ##label SAR
GENETICS
   #map_position 96.0-97.0
CLASSIFICATION   #superfamily adenovirus early E4 11K protein
KEYWORDS         early protein
SUMMARY          #length 116  #molecular-weight 13298  #checksum 6308

  Query Match           37.6%;  Score 53;  DB 4;  Length 116;
  Best Local Similarity  60.0%;  Pred. No. 1.33e+01;
  Matches     6;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db      3 rclrlkvega 12
          :|:| ||||:
Qy     11 KCVRQKVEGS 20


RESULT   20
ENTRY            Q4ADE2     #type complete
TITLE            early E4 11K protein - human adenovirus 2
ORGANISM         #formal_name Mastadenovirus h2 #common_name human adenovirus
                   2
   #note         host Homo sapiens (man)
DATE             02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
                   04-Mar-1994
ACCESSIONS       A03807
REFERENCE        A93733
   #authors      Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert,
                   F.
   #journal      Nucleic Acids Res. (1981) 9:4023-4042
   #title        Nucleotide sequence of adenovirus 2 DNA fragment encoding for
                   the carboxylic region of the fiber protein and the entire
                   E4 region.
   #cross-references MUID:82059444
   #accession    A03807
      ##molecule_type DNA
      ##residues      1-116 ##label HER
      ##note          this protein was assigned by correlating EM data and S1
                       digestion studies
GENETICS
   #map_position 96.0-97.0
CLASSIFICATION   #superfamily adenovirus early E4 11K protein
KEYWORDS         early protein
SUMMARY          #length 116  #molecular-weight 13255  #checksum 6011

  Query Match           37.6%;  Score 53;  DB 4;  Length 116;
  Best Local Similarity  60.0%;  Pred. No. 1.33e+01;
  Matches     6;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db      3 rclrlkvega 12
          :|:| ||||:
Qy     11 KCVRQKVEGS 20


RESULT   21
ENTRY            S41772     #type complete
TITLE            glycine-rich RNA-binding protein RGP-1b - wood tobacco
ORGANISM         #formal_name Nicotiana sylvestris #common_name wood tobacco
DATE             25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change
                   01-Dec-1995
ACCESSIONS       S41772
REFERENCE        S41771
   #authors      Hirose, T.; Sugita, M.; Sugiura, M.
   #journal      Nucleic Acids Res. (1993) 21:3981-3987
   #title        cDNA structure, expression and nucleic acid-binding
                   properties of three RNA-binding proteins in tobacco:
                   occurence of tissue-specific alternative splicing.
   #accession    S41772
      ##molecule_type mRNA
      ##residues      1-148 ##label HIR
      ##cross-references EMBL:D16205
CLASSIFICATION   #superfamily ribonucleoprotein repeat homology
KEYWORDS         RNA binding
FEATURE
   7-74              #domain ribonucleoprotein repeat homology #label RRM1
SUMMARY          #length 148  #molecular-weight 14655  #checksum 1944

  Query Match           37.6%;  Score 53;  DB 7;  Length 148;
  Best Local Similarity  50.0%;  Pred. No. 1.33e+01;
  Matches     6;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db     55 kdekcmrdaieg 66
          |  ||:|: :||
Qy      8 KSSKCVRQKVEG 19


RESULT   22
ENTRY            C38128     #type complete
TITLE            epithelin/granulin precursor - mouse
ALTERNATE_NAMES  acrogranin
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change
                   15-Oct-1996
ACCESSIONS       C38128; S32503; I49468
REFERENCE        A38128
   #authors      Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.;
                   McDonald, V.L.; Todaro, G.J.; Shoyab, M.
   #journal      J. Biol. Chem. (1992) 267:13073-13078
   #title        The epithelin precursor encodes two proteins with opposing
                   activities on epithelial cell growth.
   #cross-references MUID:92317004
   #accession    C38128
      ##molecule_type mRNA
      ##residues      1-589 ##label PLO
      ##cross-references GB:X62321
REFERENCE        S32503
   #authors      Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
   #journal      FEBS Lett. (1993) 322:89-94
   #title        Exon/intron organization of the gene encoding the mouse
                   epithelin/granulin precursor (acrogranin).
   #accession    S32503
      ##molecule_type DNA
      ##residues      18-349,'L',351-589 ##label BAB
REFERENCE        I48141
   #authors      Baba, T.; Hoff, H.B.
   #journal      Mol. Reprod. Dev. (1993) 34:233-243
   #title        Acrogranin, an acrosomal cysteine-rich glycoprotein, is the
                   precusor of the growth-modulating peptides, granulins, and
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                epithelins, and is expressed in somatic as well as male
                germ cells.
   #cross-references MUID:93228994
   #accession    I49468
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-250,'L',252-253,'V',255-349,'L',351-401,'SA',404-589
                       ##label RES
      ##cross-references GB:M86736; NID:g191766; CDS_PID:g191767
CLASSIFICATION   #superfamily granulin
SUMMARY          #length 589  #molecular-weight 63501  #checksum 6927

  Query Match           37.6%;  Score 53;  DB 7;  Length 589;
  Best Local Similarity  35.7%;  Pred. No. 1.33e+01;
  Matches     5;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db    560 hcsargtkclrkki 573
          | ::::::|:| |:
Qy      4 HQGTKSSKCVRQKV 17


RESULT   23
ENTRY            S43428     #type complete
TITLE            omega-crystallin - giant octopus
ORGANISM         #formal_name Octopus dofleini #common_name giant octopus
DATE             07-Sep-1994 #sequence_revision 26-May-1995 #text_change
                   26-May-1995
ACCESSIONS       S43428
REFERENCE        S43425
   #authors      Tomarev, S.I.; Zinovieva, R.D.; Piatigorsky, J.
   #journal      Biochim. Biophys. Acta (1993) 1216:245-254
   #title        Primary structure and lens-specific expression of genes for
                   an intermediate filament protein and a beta-tubulin in
                   cephalopods.
   #accession    S43428
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-591 ##label TOM
      ##cross-references EMBL:L10113
      ##note          the authors did not translate the codon for residue 1
SUMMARY          #length 591  #molecular-weight 67287  #checksum 7420

  Query Match           37.6%;  Score 53;  DB 12;  Length 591;
  Best Local Similarity  40.0%;  Pred. No. 1.33e+01;
  Matches     6;  Conservative    2;  Mismatches   7;  Indels   0;  Gaps   0;

Db     51 ishkgvtdircnrek 65
          | | |    :| |:|
Qy      2 IDHQGTKSSKCVRQK 16


RESULT   24
ENTRY            I54205     #type complete
TITLE            galactosylceramidase (EC 3.2.1.46) - human
ALTERNATE_NAMES  galactocerebrosidase; galcerase
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             24-May-1996 #sequence_revision 24-May-1996 #text_change
                   04-Oct-1996
ACCESSIONS       I54205; JC2397; PC2247; I54345
REFERENCE        I54205
   #authors      Luzi, P.; Rafi, M.A.; Wenger, D.A.
   #journal      Genomics (1995) 26:407-409
   #title        Structure and organization of the human galactocerebrosidase
                   (GALC) gene.
   #cross-references MUID:95324938
   #accession    I54205
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-669 ##label RES
      ##cross-references GB:L38559; NID:g710533; CDS_PID:g710535
REFERENCE        JC2397
   #authors      Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.;
                   Yanagihara, I.; Isegawa, Y.; Iwamatsu, A.; Okada, S.
   #journal      Biochem. Biophys. Res. Commun. (1994) 198:485-491
   #title        Krabbe disease: isolation and characterization of a
                   full-length cDNA for human galactocerebrosidase.
   #accession    JC2397
      ##molecule_type mRNA
      ##residues      1-545,'I',547-669 ##label SAK
   #accession    PC2247
      ##molecule_type protein
      ##residues      229-245;328-337;343-350;416-424;436-447;467-475;632-643;
                       661-669 ##label SA2
      ##cross-references DDBJ:D25283
REFERENCE        I54345
   #authors      Chen, Y.Q.; Rafi, M.A.; de Gala, G.; Wenger, D.A.
   #journal      Hum. Mol. Genet. (1993) 2:1841-1845
   #title        Cloning and expression of cDNA encoding human
                   galactocerebrosidase, the enzyme deficient in globoid cell
                   leukodystrophy.
   #cross-references MUID:94108435
   #accession    I54345
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-545,'I',547-669 ##label RE2
      ##cross-references GB:L23116; NID:g431309; CDS_PID:g431310
COMMENT      This enzyme hydrolyzes the galactose ester bonds of
               galactosylceramide, galactosylsphingosine,
               monogalactosyldiglyceride and lactosylceramide.
GENETICS
   #gene         GDB:GALC
      ##cross-references GDB:119970
   #map_position 14q31-14q31
   #introns      49/3; 72/3; 94/1; 132/1; 178/3; 191/3; 235/2; 287/2; 329/1;
                   371/3; 401/3; 430/3; 481/1; 541/2; 596/1; 621/3
KEYWORDS         glycoprotein; glycosidase; hydrolase
FEATURE
   1-26               #domain signal sequence #status predicted #label SIG\
   27-669             #product galactosylceramidase #status predicted #label
                        MAT\
   127,363,387,540,
   543,586            #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY          #length 669  #molecular-weight 75135  #checksum 818

  Query Match           37.6%;  Score 53;  DB 13;  Length 669;
  Best Local Similarity  42.9%;  Pred. No. 1.33e+01;
  Matches     6;  Conservative    4;  Mismatches   4;  Indels   0;  Gaps   0;

Db    367 iietmshkhskcir 380
          :|:  : | |||:|
Qy      1 VIDHQGTKSSKCVR 14


RESULT   25
ENTRY            PFHUGA     #type complete
TITLE            platelet-derived growth factor receptor alpha precursor -
                   human
CONTAINS         protein-tyrosine kinase (EC 2.7.1.112)
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
                   13-Sep-1996
ACCESSIONS       A40162; A32941
REFERENCE        A40162
   #authors      Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,
                   W.; Kraus, M.; Pierce, J.; Aaronson, S.
   #journal      Science (1989) 243:800-804
   #title        Isolation of a novel receptor cDNA establishes the existence
                   of two PDGF receptor genes.
   #cross-references MUID:89130149
   #accession    A40162
      ##molecule_type mRNA
      ##residues      1-1089 ##label MATS
      ##cross-references GB:M21574
REFERENCE        A32941
   #authors      Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Heldin,
```

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                  C.H.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4917-4921
   #title         cDNA cloning and expression of the human A-type
                    platelet-derived growth factor (PDGF) receptor establishes
                    structural similarity to the B-type PDGF receptor.
   #cross-references MUID:89296915
   #accession     A32941
      ##molecule_type mRNA
      ##residues      1-1089 ##label CLA
      ##cross-references GB:M22734
COMMENT     The extracellular domain is predicted to include five
              immunoglobulin-like domains.
GENETICS
   #gene          GDB:PDGFRA
      ##cross-references GDB:120267
   #map_position 4q11-4q12
CLASSIFICATION   #superfamily macrophage colony-stimulating factor 1 receptor;
                    immunoglobulin homology; protein kinase homology
KEYWORDS         ATP; autophosphorylation; dimer; glycoprotein;
                    phosphoprotein; phosphotransferase; transmembrane protein;
                    tyrosine-specific protein kinase
FEATURE
   1-24              #domain signal sequence #status predicted #label SIG\
   25-1089           #product platelet-derived growth factor receptor alpha
                       #status predicted #label MAT\
   25-524            #domain extracellular #status predicted #label EXT\
   42-102            #domain immunoglobulin homology #label IMM1\
   143-191           #domain immunoglobulin homology #label IMM2\
   228-292           #domain immunoglobulin homology #label IMM3\
   428-503           #domain immunoglobulin homology #label IMM4\
   525-548           #domain transmembrane #status predicted #label TMM\
   549-1089          #domain intracellular #status predicted #label INT\
   591-957           #domain protein kinase homology #label KIN\
   599-607           #region protein kinase ATP-binding motif\
   42,76,103,179,353,
   359,458,468       #binding_site carbohydrate (Asn) (covalent) #status
                       predicted\
   49-100,150-189,
   235-290,435-501   #disulfide_bonds #status predicted\
   627               #active_site Lys #status predicted\
   849               #binding_site phosphate (Tyr) (covalent) (by
                       autophosphorylation) #status predicted
SUMMARY          #length 1089  #molecular-weight 122668  #checksum 4547

  Query Match           37.6%;  Score 53;  DB 1;  Length 1089;
  Best Local Similarity  38.1%;  Pred. No. 1.33e+01;
  Matches     8;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    421 vddhhgstgggtvrctaegtp 441
          | ||:|: ::  ||   ||::
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


Search completed: Tue Jul 29 07:32:10 1997
Job time : 36 secs.
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Release 2.1D John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 29 07:30:59 1997; MasPar time 2.33 Seconds
190.965 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 26.425; Variance 29.915; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	141	100.0	1676	2	CO5_HUMAN	COMPLEMENT C5 PRECURS	1.16e-24
2	69	48.9	1680	2	CO5_MOUSE	COMPLEMENT C5 PRECURS	7.22e-04
3	59	41.8	943	5	IROA_NEIME	IRON-REGULATED OUTER	1.65e-01
4	59	41.8	1002	11	YEMA_DROME	YEMANUCLEIN-ALPHA.	1.65e-01
5	57	40.4	116	8	RL34_HUMAN	60S RIBOSOMAL PROTEIN	4.57e-01
6	57	40.4	264	2	CSH_ARTSP	N-CARBAMOYLSARCOSINE	4.57e-01
7	56	39.7	537	9	SP70_DICDI	SPORE COAT PROTEIN SP	7.54e-01
8	56	39.7	573	4	GLB1_MAIZE	GLOBULIN-1 S ALLELE P	7.54e-01
9	56	39.7	1357	8	RPOB_PSEPU	DNA-DIRECTED RNA POLY	7.54e-01
10	55	39.0	775	11	YTX1_XENLA	TRANSPOSON TX1 HYPOTH	1.24e+00
11	54	38.3	148	2	COTZ_BACSU	SPORE COAT PROTEIN Z.	2.01e+00
12	54	38.3	818	3	DAP2_YEAST	DIPEPTIDYL AMINOPEPTI	2.01e+00
13	54	38.3	1039	11	YR71_CAEEL	HYPOTHETICAL 118.2 KD	2.01e+00
14	53	37.6	116	3	E411_ADE05	PROBABLE EARLY E4 11	3.25e+00
15	53	37.6	116	3	E411_ADE02	PROBABLE EARLY E4 11	3.25e+00
16	53	37.6	589	4	GRN_MOUSE	GRANULINS PRECURSOR (	3.25e+00
17	53	37.6	669	4	GALC_HUMAN	GALACTOCEREBROSIDASE	3.25e+00
18	53	37.6	1089	7	PGDS_HUMAN	ALPHA PLATELET-DERIVE	3.25e+00
19	52	36.9	329	3	ESG2_TRYBB	VSG EXPRESSION SITE-A	5.22e+00
20	52	36.9	354	7	OCD_AGRT5	ORNITHINE CYCLODEAMIN	5.22e+00
21	52	36.9	455	7	P2X5_RAT	P2X PURINOCEPTOR 5 (A	5.22e+00
22	51	36.2	121	11	YIF2_YEAST	PROBABLE 60S RIBOSOMA	8.32e+00
23	51	36.2	337	10	VP67_NPVGM	MAJOR ENVELOPE GLYCOP	8.32e+00
24	51	36.2	337	1	ADH1_ZYMMO	ALCOHOL DEHYDROGENASE	8.32e+00
25	51	36.2	462	5	KPY1_ECOLI	PYRUVATE KINASE I (EC	8.32e+00
26	51	36.2	512	10	VP67_NPVAC	MAJOR ENVELOPE GLYCOP	8.32e+00
27	51	36.2	574	3	ESTR_SALIR	ESTROGEN RECEPTOR (ER	8.32e+00
28	51	36.2	588	4	GRN_RAT	GRANULINS PRECURSOR (	8.32e+00
29	51	36.2	1056	6	MUC5_HUMAN	TRACHEOBRONCHIAL MUCI	8.32e+00
30	51	36.2	1651	10	VIT6_CAEEL	VITELLOGENIN 6 PRECUR	8.32e+00
31	51	36.2	1678	2	CLH_DROME	CLATHRIN HEAVY CHAIN.	8.32e+00
32	50	35.5	123	8	RL14_HAEIN	50S RIBOSOMAL PROTEIN	1.32e+01
33	50	35.5	171	11	YJB6_YEAST	HYPOTHETICAL 19.7 KD	1.32e+01
34	50	35.5	192	10	Y045_NPVAC	HYPOTHETICAL 22.7 KD	1.32e+01
35	50	35.5	296	8	RBSB_ECOLI	D-RIBOSE-BINDING PERI	1.32e+01
36	50	35.5	296	8	RBSB_SALTY	D-RIBOSE-BINDING PERI	1.32e+01
37	50	35.5	301	9	TRT2_CHICK	TROPONIN T, CARDIAC M	1.32e+01
38	50	35.5	410	1	BEDA_PSEPU	BENZENE 1,2-DIOXYGENA	1.32e+01
39	50	35.5	592	5	INVA_DAUCA	BETA-FRUCTOFURANOSIDA	1.32e+01
40	50	35.5	1010	10	WNT5_DROME	PROTEIN DWNT-5 PRECUR	1.32e+01
41	49	34.8	72	10	VSM0_TRYBB	VARIANT SURFACE GLYCO	2.06e+01
42	49	34.8	99	5	ITI2_SINAL	TRYPSIN INHIBITOR 2 P	2.06e+01
43	49	34.8	121	8	RK14_ODOSI	CHLOROPLAST 50S RIBOS	2.06e+01
44	49	34.8	122	8	RK14_PORPU	CHLOROPLAST 50S RIBOS	2.06e+01
45	49	34.8	122	8	RL14_THETH	50S RIBOSOMAL PROTEIN	2.06e+01
46	49	34.8	175	10	Y04G_MYCTU	HYPOTHETICAL 19.3 KD	2.06e+01
47	49	34.8	220	1	ANTA_HYDMA	ANTISTASIN PRECURSOR	2.06e+01
48	49	34.8	222	8	PSPA_ECOLI	PHAGE SHOCK PROTEIN A	2.06e+01
49	49	34.8	267	11	YD6A_SCHPO	HYPOTHETICAL 30.6 KD	2.06e+01
50	49	34.8	424	11	ZFP1_MOUSE	ZINC FINGER PROTEIN Z	2.06e+01
51	49	34.8	429	6	NCAP_HANTV	NUCLEOCAPSID PROTEIN	2.06e+01
52	49	34.8	487	5	HR3_DROME	PROBABLE NUCLEAR HORM	2.06e+01
53	49	34.8	509	10	VP67_NPVCF	MAJOR ENVELOPE GLYCOP	2.06e+01
54	49	34.8	591	4	FUCI_ECOLI	L-FUCOSE ISOMERASE (E	2.06e+01
55	49	34.8	660	2	CIK4_BOVIN	POTASSIUM CHANNEL PRO	2.06e+01
56	49	34.8	732	9	TRI6_ECOLI	TRAI PROTEIN.	2.06e+01
57	49	34.8	752	6	NSF2_DROME	VESICULAR-FUSION PROT	2.06e+01
58	49	34.8	784	4	GCF_HUMAN	GC-RICH SEQUENCE DNA-	2.06e+01
59	49	34.8	1088	7	PGDS_RAT	ALPHA PLATELET-DERIVE	2.06e+01
60	49	34.8	1323	6	NME4_MOUSE	GLUTAMATE (NMDA) RECE	2.06e+01
61	49	34.8	1451	1	A2MH_MOUSE	MURINOGLOBULIN 2 PREC	2.06e+01
62	49	34.8	1476	1	A2MG_MOUSE	MURINOGLOBULIN 1 PREC	2.06e+01
63	48	34.0	233	8	RL1_ECOLI	50S RIBOSOMAL PROTEIN	3.21e+01
64	48	34.0	339	9	TF3A_BUFAM	TRANSCRIPTION FACTOR	3.21e+01
65	48	34.0	353	6	NOV_COTJA	NOV PROTEIN PRECURSOR	3.21e+01
66	48	34.0	376	3	DUT_HSV6Z	DEOXYURIDINE 5'-TRIPH	3.21e+01
67	48	34.0	399	7	P2X1_HUMAN	P2X PURINOCEPTOR 1 (A	3.21e+01
68	48	34.0	481	3	DPOL_HPBVW	DNA POLYMERASE (EC 2.	3.21e+01
69	48	34.0	683	9	SFP1_YEAST	ZINC FINGER PROTEIN S	3.21e+01
70	48	34.0	791	5	KDGG_HUMAN	DIACYLGLYCEROL KINASE	3.21e+01
71	48	34.0	845	3	DPOL_HPBV2	DNA POLYMERASE (EC 2.	3.21e+01
72	48	34.0	873	7	PC1_HUMAN	PLASMA-CELL MEMBRANE	3.21e+01
73	48	34.0	953	11	YNM7_YEAST	HYPOTHETICAL 109.8 KD	3.21e+01
74	48	34.0	974	1	ATXB_LEIDO	PROBABLE E1-E2 TYPE C	3.21e+01
75	48	34.0	974	1	ATXA_LEIDO	PROBABLE E1-E2 TYPE C	3.21e+01
76	48	34.0	1216	1	ATC2_YEAST	PROBABLE CALCIUM-TRAN	3.21e+01
77	48	34.0	1296	1	ASA1_ENTFA	AGGREGATION SUBSTANCE	3.21e+01
78	48	34.0	1350	10	VG72_HSV11	HYPOTHETICAL GENE 72	3.21e+01
79	47	33.3	47	8	RK14_VIGUN	CHLOROPLAST 50S RIBOS	4.95e+01
80	47	33.3	100	11	YHBQ_ECOLI	HYPOTHETICAL 11.3 KD	4.95e+01
81	47	33.3	122	8	RK14_CHLRE	CHLOROPLAST 50S RIBOS	4.95e+01
82	47	33.3	123	8	RK14_TOBAC	CHLOROPLAST 50S RIBOS	4.95e+01
83	47	33.3	157	8	RS7_CHLTR	30S RIBOSOMAL PROTEIN	4.95e+01
84	47	33.3	179	11	YPUI_BACSU	HYPOTHETICAL 20.4 KD	4.95e+01
85	47	33.3	277	5	KNOB_PLAFD	KNOB-ASSOCIATED HISTI	4.95e+01
86	47	33.3	343	6	NOV_XENLA	NOV PROTEIN HOMOLOG P	4.95e+01
87	47	33.3	348	11	YLW1_CAEEL	HYPOTHETICAL 41.0 KD	4.95e+01
88	47	33.3	394	3	EFTU_BORBU	ELONGATION FACTOR TU	4.95e+01
89	47	33.3	473	5	KNOB_PLAFA	KNOB-ASSOCIATED HISTI	4.95e+01
90	47	33.3	491	2	CPH1_CHICK	CYTOCHROME P450 IIH1	4.95e+01
91	47	33.3	498	4	GAG_HV1OY	GAG POLYPROTEIN (CONT	4.95e+01
92	47	33.3	499	4	GAG_HV1Y2	GAG POLYPROTEIN (CONT	4.95e+01
93	47	33.3	634	5	KNOB_PLAFG	KNOB-ASSOCIATED HISTI	4.95e+01
94	47	33.3	634	5	KNOB_PLAFX	KNOB-ASSOCIATED HISTI	4.95e+01
95	47	33.3	727	7	NUAM_BOVIN	NADH-UBIQUINONE OXIDO	4.95e+01

96	47	33.3	727	7	NUAM_HUMAN	NADH-UBIQUINONE OXIDO	4.95e+01
97	47	33.3	763	3	DPOL_HPBVP	DNA POLYMERASE (EC 2.	4.95e+01
98	47	33.3	1080	3	CYA7_HUMAN	ADENYLATE CYCLASE, TY	4.95e+01
99	47	33.3	1099	3	CYA7_MOUSE	ADENYLATE CYCLASE, TY	4.95e+01
100	47	33.3	1500	1	AT7A_HUMAN	COPPER-TRANSPORTING A	4.95e+01

ALIGNMENTS

```
RESULT    1
ID   CO5_HUMAN      STANDARD;      PRT;  1676 AA.
AC   P01031;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN).
GN   C5.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91079575.
RA   HAVILAND D.L., HAVILAND J.C., FLEISCHER D.T., HUNT A., WETSEL R.A.;
RL   J. IMMUNOL. 146:362-368(1991).
RN   [2]
RP   SEQUENCE OF 412-1676 FROM N.A.
RX   MEDLINE; 88209511.
RA   WETSEL R.A., LEMONS R.S., LEBEAU M.M., BARNUM S.R., NOACK D.,
RA   TACK B.F.;
RL   BIOCHEMISTRY 27:1474-1482(1988).
RN   [3]
RP   SEQUENCE OF 412-902 FROM N.A.
RX   MEDLINE; 85130937.
RA   LUNDWALL A.B., WETSEL R.A., KRISTENSEN T., WHITEHEAD A.S.,
RA   WOODS D.E., OGDEN R.C., COLTEN H.R., TACK B.F.;
RL   J. BIOL. CHEM. 260:2108-2112(1985).
RN   [4]
RP   SEQUENCE OF 678-751.
RX   MEDLINE; 79005687.
RA   FERNANDEZ H.N., HUGLI T.E.;
RL   J. BIOL. CHEM. 253:6955-6964(1978).
RN   [5]
RP   SEQUENCE OF 678-751 FROM N.A.
RX   MEDLINE; 91144547.
RA   BOHNSACK J.F., MOLLISON K.W., BUKO A.M., ASHWORTH J.C., HILL H.R.;
RL   BIOCHEM. J. 273:635-640(1991).
RN   [6]
RP   STRUCTURE BY NMR OF C5A.
RX   MEDLINE; 88309754.
RA   ZUIDERWEG E.R., MOLLISON K.W., HENKIN J., CARTER G.W.;
RL   BIOCHEMISTRY 27:3568-3580(1988).
RN   [7]
RP   STRUCTURE BY NMR OF C5A.
RX   MEDLINE; 89207527.
RA   ZUIDERWEG E.R., NETTESHEIM D.G., MOLLISON K.W., CARTER G.W.;
RL   BIOCHEMISTRY 28:172-185(1989).
RN   [8]
RP   STRUCTURE BY NMR OF C5A.
RX   MEDLINE; 89274164.
RA   ZUIDERWEG E.R., FESIK S.W.;
RL   BIOCHEMISTRY 28:2387-2391(1989).
CC   -!- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC       SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
CC       INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC       FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC
CC       COMPLEX IS ASSEMBLED.
CC   -!- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
CC       RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC       BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
CC       RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA'
CC       CHAIN).
CC   -!- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
CC   -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC       C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC       INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC       PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC       BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC       POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC       MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC   -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
CC       ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
CC   -!- SIMILARITY: CONTAINS ONE ANAPHYLATOXIN-LIKE DOMAIN.
DR   EMBL; M57729; G179983; -.
DR   EMBL; M65134; G179692; -.
DR   PIR; A40075; C5HU.
DR   PIR; S15121; S15121.
DR   HSSP; P01032; 1C5A.
DR   MIM; 120900; -.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN.
KW   COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
KW   PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; INFLAMMATORY RESPONSE;
KW   SIGNAL; POLYMORPHISM.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    673       COMPLEMENT C5 BETA CHAIN.
FT   PROPEP      674    677
FT   CHAIN       678   1676       COMPLEMENT C5 ALPHA CHAIN.
FT   PEPTIDE     678    751       C5A ANAPHYLATOXIN.
FT   CHAIN       752   1676       C5B (ALPHA').
FT   DOMAIN      698    732       ANAPHYLATOXIN-LIKE.
FT   DISULFID    698    724
FT   DISULFID    699    731
FT   DISULFID    711    732
FT   CARBOHYD    741    741
FT   CARBOHYD    911    911       POTENTIAL.
FT   CARBOHYD   1115   1115       POTENTIAL.
FT   CARBOHYD   1630   1630       POTENTIAL.
FT   VARIANT     518    518       F -> S.
SQ   SEQUENCE   1676 AA;  188331 MW;  9D5C6E59 CRC32;

  Query Match          100.0%;  Score 141;  DB 2;  Length 1676;
  Best Local Similarity 100.0%;  Pred. No. 1.16e-24;
  Matches    21;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    872 vidhqgtkssksvrqkvegss 892
          |||||||||||||||||||||
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT    2
ID   CO5_MOUSE      STANDARD;      PRT;  1680 AA.
AC   P06684;
DT   01-JAN-1988 (REL. 06, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN).
GN   C5.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90153853.
RA   WETSEL R.A., FLEISCHER D.T., HAVILAND D.L.;
RL   J. BIOL. CHEM. 265:2435-2440(1990).
RN   [2]
RP   SEQUENCE OF 41-1680 FROM N.A.
RX   MEDLINE; 87185363.
RA   WETSEL R.A., OGATA R.T., TACK B.F.;
RL   BIOCHEMISTRY 26:737-743(1987).
CC   -!- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC       SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
CC       INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC       FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC
CC       COMPLEX IS ASSEMBLED.
CC   -!- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
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CC       RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC       BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
CC       RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA'
CC       CHAIN).
CC   -!- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
CC   -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC       C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC       INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC       PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC       BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC       POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC       MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC   -!- SIMILARITY: CONTAINS ONE ANAPHYLATOXIN-LIKE DOMAIN.
DR   EMBL; M35525; G309124; -.
DR   EMBL; M35526; G309123; -.
DR   PIR; A27538; A27538.
DR   PIR; A35530; A35530.
DR   HSSP; P01032; 1C5A.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN.
KW   COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
KW   PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; INFLAMMATORY RESPONSE;
KW   SIGNAL.
FT   SIGNAL        1     18
FT   CHAIN        19   1680       COMPLEMENT C5.
FT   CHAIN        19    674       COMPLEMENT C5 BETA CHAIN.
FT   PROPEP      675    678
FT   CHAIN       679   1680       COMPLEMENT C5 ALPHA CHAIN.
FT   PEPTIDE     679    755       C5A ANAPHYLATOXIN.
FT   CHAIN       756   1680       C5B (ALPHA').
FT   DOMAIN      702    736       ANAPHYLATOXIN-LIKE.
FT   DISULFID    702    728       BY SIMILARITY.
FT   DISULFID    703    735       BY SIMILARITY.
FT   DISULFID    715    736       BY SIMILARITY.
FT   CARBOHYD    427    427       POTENTIAL.
FT   CARBOHYD    915    915       POTENTIAL.
FT   CARBOHYD   1119   1119       POTENTIAL.
FT   CARBOHYD   1633   1633       POTENTIAL.
FT   VARIANT     216    216       Y -> L (IN DEFECTIVE VARIANT C5D).
FT   VARIANT     217   1680       MISSING (IN DEFECTIVE VARIANT C5D).
SQ   SEQUENCE   1680 AA;  188877 MW;  AA17044B CRC32;

  Query Match           48.9%;  Score 69;  DB 2;  Length 1680;
  Best Local Similarity  47.1%;  Pred. No. 7.22e-04;
  Matches     8;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db    880 htsrpsrcvfqriegss 896
          : :::|:|| |::|||| 
Qy      5 QGTKSSKCVRQKVEGSS 21


RESULT    3
ID   IROA_NEIME     STANDARD;      PRT;   943 AA.
AC   Q06379;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   IRON-REGULATED OUTER MEMBRANE PROTEIN A PRECURSOR.
GN   IROA.
OS   NEISSERIA MENINGITIDIS.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   NEISSERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BNVC;
RX   MEDLINE; 94011384.
RA   PETTERSSON A., VAN DER LEY P., POOLMAN J.T., TOMMASSEN J.;
RL   INFECT. IMMUN. 61:4724-4733(1993).
CC   -!- FUNCTION: UNKNOWN. MAY BE AN IRON-SIDEROPHORE RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
CC   -!- INDUCTION: BY IRON-STARVATION CONDITIONS.
CC   -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
DR   EMBL; X69214; G45064; -.
DR   PROSITE; PS00430; TONB_DEPENDENT_REC_1.
DR   PROSITE; PS01156; TONB_DEPENDENT_REC_2.
KW   OUTER MEMBRANE; IRON TRANSPORT; TRANSPORT; TONB BOX; SIGNAL; RECEPTOR.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    943       IRON-REGULATED OUTER MEMBRANE PROTEIN A.
FT   SIMILAR     826    943       TONB C-TERMINAL BOX.
SQ   SEQUENCE   943 AA;  105424 MW;  16644948 CRC32;

  Query Match           41.8%;  Score 59;  DB 5;  Length 943;
  Best Local Similarity  50.0%;  Pred. No. 1.65e-01;
  Matches     7;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db    595 rsrkcvprkingsn 608
          :| ||| :|::||:
Qy      8 KSSKCVRQKVEGSS 21


RESULT    4
ID   YEMA_DROME     STANDARD;      PRT;  1002 AA.
AC   P25992;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   YEMANUCLEIN-ALPHA.
GN   YEMA OR YG4.5.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RX   MEDLINE; 92297435.
RA   AIT-AHMED O., BELLON B., CAPRI M., JOBLET C., THOMAS-DELAAGE M.;
RL   MECH. DEV. 37:69-80(1992).
CC   -!- FUNCTION: MAY PLAY A KEY ROLE IN EGG ORGANIZATION. IT MAY BE A
CC       TRANSCRIPTIONAL REGULATOR.
CC   -!- PTM: THE N-TERMINAL IS BLOCKED.
CC   -!- TISSUE SPECIFICITY: OOCYTE-SPECIFIC.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL OOGENIC STAGES.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; X63503; G8838; -.
DR   PIR; S22146; S22146.
DR   FLYBASE; FBGN0005596; YEM-ALPHA.
KW   NUCLEAR PROTEIN; DNA-BINDING; REPEAT.
FT   DOMAIN       80     85       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      207    217       POLY-SER.
FT   DOMAIN      219    261       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      230    253       2 X 12 AA TANDEM REPEATS.
FT   REPEAT      230    241       1.
FT   REPEAT      242    253       2.
FT   VARIANT     698    698       S -> L (IN CDNA SEQUENCE).
SQ   SEQUENCE   1002 AA;  109310 MW;  955FD2C1 CRC32;

  Query Match           41.8%;  Score 59;  DB 11;  Length 1002;
  Best Local Similarity  50.0%;  Pred. No. 1.65e-01;
  Matches     6;  Conservative    5;  Mismatches   1;  Indels   0;  Gaps   0;

Db     47 tktakcirikld 58
          ||::||:| |::
Qy      7 TKSSKCVRQKVE 18


RESULT    5
ID   RL34_HUMAN     STANDARD;      PRT;   116 AA.
AC   P49207;
DT   01-FEB-1996 (REL. 33, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   60S RIBOSOMAL PROTEIN L34.
GN   RPL34.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   TISSUE=OVARY;
RX   MEDLINE; 96039267.
RA   ROMMENS J.M., DUROCHER F., MCARTHUR J., TONIN P., LEBLANC J.F.,
RA   ALLEN T., SAMSON C., FERRI L., NAROD S., MORGAN K., SIMARD J.;
RL   GENOMICS 28:530-542(1995).
CC   -!- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
DR   EMBL; L38941; G1008856; -.
KW   RIBOSOMAL PROTEIN.
FT   INIT_MET      0      0       BY SIMILARITY.
SQ   SEQUENCE   116 AA;  13174 MW;  490F4AF1 CRC32;

  Query Match           40.4%;  Score 57;  DB 8;  Length 116;
  Best Local Similarity  41.7%;  Pred. No. 4.57e-01;
  Matches     5;  Conservative    6;  Mismatches   1;  Indels   0;  Gaps   0;

Db     79 gsmcakcvrdri 90
          |:: :||||::: 
Qy      6 GTKSSKCVRQKV 17


RESULT    6
ID   CSH_ARTSP      STANDARD;      PRT;   264 AA.
AC   P32400;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   N-CARBAMOYLSARCOSINE AMIDASE (EC 3.5.1.59) (N-CARBAMOYLSARCOSINE
DE   AMIDOHYDROLASE) (CSHASE).
OS   ARTHROBACTER SP.
OC   PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS; CORYNEFORM GROUP.
RN   [1]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 184 AND 232.
RX   MEDLINE; 92389321.
RA   ROMAO M.J., TURK D., GOMIS-RUETH F.-X., HUBER R.;
RL   J. MOL. BIOL. 226:1111-1130(1992).
CC   -!- CATALYTIC ACTIVITY: N-CARBAMOYLSARCOSINE + H(2)O = SARCOSINE +
CC       CO(2) + NH(3).
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- COFACTOR: ONE SULFATE ION PER SUBUNIT.
CC   -!- PATHWAY: DEGRADATION OF CREATININE TO GLYCINE.
DR   PIR; S28969; S28969.
DR   PDB; 1NBA; 22-JUN-94.
KW   HYDROLASE; 3D-STRUCTURE.
FT   ACT_SITE    177    177       INVOLVED IN HYDROLYSIS OF THE SUBSTRATE.
SQ   SEQUENCE   264 AA;  29057 MW;  81A56865 CRC32;

  Query Match           40.4%;  Score 57;  DB 2;  Length 264;
  Best Local Similarity  40.0%;  Pred. No. 4.57e-01;
  Matches     6;  Conservative    5;  Mismatches   4;  Indels   0;  Gaps   0;

Db    171 gataagcvrhtveda 185
          |: :: |||: || :
Qy      6 GTKSSKCVRQKVEGS 20


RESULT    7
ID   SP70_DICDI     STANDARD;      PRT;   537 AA.
AC   P15269; P08126;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   SPORE COAT PROTEIN SP70 PRECURSOR (BEEJIN PROTEIN).
GN   COTB.
OS   DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
OC   EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
OC   EUMYCETOZOA; DICTYOSTELIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90097939.
RA   FOSNAUGH K.L., LOOMIS W.F.;
RL   MOL. CELL. BIOL. 9:5215-5218(1989).
RN   [2]
RP   PRELIMINARY SEQUENCE OF 72-170 FROM N.A.
RX   MEDLINE; 87057653.
RA   GOMER R.H., DATTA S., FIRTEL R.A.;
RL   J. CELL BIOL. 103:1999-2015(1986).
DR   EMBL; M26238; G167889; -.
DR   PIR; B33485; B33485.
DR   PIR; B25439; B25439.
DR   DICTYDB; DD03009; COTB.
KW   GLYCOPROTEIN; PHOSPHORYLATION; REPEAT; SPORULATION; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    537       SPORE COAT PROTEIN SP70.
FT   DOMAIN      182    250       SER/THR-RICH.
FT   DOMAIN      190    248       5.5 X 11 AA TANDEM REPEATS.
FT   REPEAT      190    200       1.
FT   REPEAT      191    211       2.
FT   REPEAT      212    222       3.
FT   REPEAT      223    233       4.
FT   REPEAT      234    244       5.
FT   REPEAT      245    248       6 (INCOMPLETE).
FT   REPEAT      256    263       PRESPORE MOTIF.
FT   REPEAT      284    291       PRESPORE MOTIF.
FT   REPEAT      364    371       PRESPORE MOTIF.
FT   CARBOHYD     97     97       POTENTIAL.
SQ   SEQUENCE   537 AA;  56650 MW;  5D59CBAC CRC32;

  Query Match           39.7%;  Score 56;  DB 9;  Length 537;
  Best Local Similarity  54.5%;  Pred. No. 7.54e-01;
  Matches     6;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;

Db    291 kngecirdkve 301
          |:: |:|:||| 
Qy      8 KSSKCVRQKVE 18


RESULT    8
ID   GLB1_MAIZE     STANDARD;      PRT;   573 AA.
AC   P15590;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
GN   GLB1.
OS   ZEA MAYS (MAIZE).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
OC   CYPERALES; GRAMINEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. INBRED LINE VA26;
RA   BELANGER F.C., KRIZ A.L.;
RL   PLANT PHYSIOL. 91:636-643(1989).
RN   [2]
RP   SEQUENCE OF 87-100.
RX   MEDLINE; 89374022.
RA   KRIZ A.L.;
RL   BIOCHEM. GENET. 27:239-251(1989).
CC   -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC       CONVICILIN, CONGLYCININ, ETC.).
CC   -!- POLYMORPHISM: THE THREE MOST COMMONLY OCCURING GLB1 ALLELES HAVE
CC       THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
CC       PROTEINS, RESPECTIVELY.
CC   -!- PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
CC       MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
DR   EMBL; M24845; G168481; -.
DR   HSSP; P02853; 1CAU.
DR   MAIZEDB; 30181; -.
KW   SEED STORAGE PROTEIN; SIGNAL.
FT   SIGNAL        1     18       OR 21 (POTENTIAL).
FT   PROPEP       19     86
FT   CHAIN        87    573       GLOBULIN-1 S.
FT   CARBOHYD    349    349       POTENTIAL.
SQ   SEQUENCE   573 AA;  65029 MW;  7E755E20 CRC32;

  Query Match           39.7%;  Score 56;  DB 4;  Length 573;
  Best Local Similarity  58.3%;  Pred. No. 7.54e-01;
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  Matches     7;  Conservative     3;  Mismatches   2;  Indels    0;  Gaps    0;

Db      32 hgghksgrcvrr 43
           | | ||::|||:
Qy       4 HQGTKSSKCVRQ 15


RESULT    9
ID   RPOB_PSEPU     STANDARD;      PRT;  1357 AA.
AC   P19175;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
DE   BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
GN   RPOB.
OS   PSEUDOMONAS PUTIDA.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   PSEUDOMONADACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BORODIN A.M., DANILKOVICH A.V., ALLIKMETS R.L., ROSTAPSHOV V.M.,
RA   CHERNOV I.P., AZHIKINA T.L., MONASTYRSKAYA S., SVERDLOV D.;
RL   DOKL. BIOCHEM. 302:1261-1265(1988).
RN   [2]
RP   SEQUENCE OF 1036-1357 FROM N.A.
RX   MEDLINE; 89117617.
RA   BORODIN A.M., DANILKOVICH A.V., CHERNOV I.P., AZHYKINA T.L.,
RA   ROSTAPSHOV V.M., MONASTYRSKAYA G.S.;
RL   BIOORG. KHIM. 14:1179-1182(1988).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC       ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC       BETA' CHAIN.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
DR   EMBL; X15849; G45729; -.
DR   EMBL; M38319; G151547; -.
KW   TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE.
FT   CONFLICT    1180   1180       T -> N (IN REF. 2).
FT   CONFLICT    1184   1184       I -> V (IN REF. 2).
FT   CONFLICT    1236   1236       F -> S (IN REF. 2).
SQ   SEQUENCE    1357 AA;  151305 MW;  BBF88A37 CRC32;

  Query Match           39.7%;  Score 56;  DB 8;  Length 1357;
  Best Local Similarity  41.2%;  Pred. No. 7.54e-01;
  Matches     7;  Conservative     4;  Mismatches   6;  Indels    0;  Gaps    0;

Db     450 idhlgnrrvrcvgemae 466
           ||| | :  :|| :: |
Qy       2 IDHQGTKSSKCVRQKVE 18


RESULT   10
ID   YTX1_XENLA     STANDARD;      PRT;   775 AA.
AC   P14380;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   TRANSPOSON TX1 HYPOTHETICAL 82 KD PROTEIN (ORF 1).
OS   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89384562.
RA   GARRETT J.E., KNUTZON D.S., CARROLL D.;
RL   MOL. CELL. BIOL. 9:3018-3027(1989).
DR   EMBL; M26915; G214845; -.
DR   PIR; A32494; A32494.
KW   HYPOTHETICAL PROTEIN; TRANSPOSABLE ELEMENT.

SQ   SEQUENCE   775 AA;  82355 MW;  9738B05A CRC32;

  Query Match           39.0%;  Score 55;  DB 11;  Length 775;
  Best Local Similarity  46.7%;  Pred. No. 1.24e+00;
  Matches     7;  Conservative     5;  Mismatches   3;  Indels    0;  Gaps    0;

Db     617 sntskcvssevegtp 631
           :::|||| |||::
Qy       7 TKSSKCVRQKVEGSS 21


RESULT   11
ID   COTZ_BACSU     STANDARD;      PRT;   148 AA.
AC   Q08312;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   SPORE COAT PROTEIN Z.
GN   COTZ.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / JH642;
RX   MEDLINE; 93285989.
RA   ZHANG J., FITZ-JAMES P.C., ARONSON A.I.;
RL   J. BACTERIOL. 175:3757-3766(1993).
CC   -!- SUBCELLULAR LOCATION: SPORE OUTER COAT.
CC   -!- SUBUNIT: DISULFIDE CROSS-LINKED EITHER TO ITSELF OR TO COTY.
CC   -!- SIMILARITY: TO COTY.
DR   EMBL; L10116; G304149; -.
DR   PIR; E47119; E47119.
DR   SUBTILIST; BG10500; COTZ.
KW   SPORULATION.
SQ   SEQUENCE   148 AA;  16534 MW;  B5442F5E CRC32;

  Query Match           38.3%;  Score 54;  DB 2;  Length 148;
  Best Local Similarity  63.6%;  Pred. No. 2.01e+00;
  Matches     7;  Conservative     2;  Mismatches   2;  Indels    0;  Gaps    0;

Db       4 ktsscvreave 14
           |:| |||: ||
Qy       8 KSSKCVRQKVE 18


RESULT   12
ID   DAP2_YEAST     STANDARD;      PRT;   818 AA.
AC   P18962;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   DIPEPTIDYL AMINOPEPTIDASE B (EC 3.4.14.-) (DPAP B) (YSCV).
GN   DAP2 OR YHR028C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89174971.
RA   ROBERTS C.J., POHLIG G., ROTHMAN J.H., STEVENS T.H.;
RL   J. CELL BIOL. 108:1363-1373(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RX   MEDLINE; 94378003.
RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
RA   NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA   VAUDIN M.;
RL   SCIENCE 265:2077-2082(1994).
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOME-LIKE
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CC       VACUOLES.
CC   -!- SIMILARITY: TO DPAP A.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC       PROLYL OLIGOPEPTIDASE FAMILY.
DR   EMBL; X15484; G3660; -.
DR   EMBL; U10399; G500698; -.
DR   PIR; A30107; A30107.
DR   PIR; S46780; S46780.
DR   LISTA; SC00265; DAP2.
DR   SGD; L0000483; DAP2.
DR   PROSITE; PS00708; PRO_ENDOPEP_SER.
KW   HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW   SIGNAL-ANCHOR.
FT   DOMAIN        1     29       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     30     45       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT   DOMAIN       46    818       LUMENAL (POTENTIAL).
FT   ACT_SITE    679    679       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    756    756       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    789    789       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   CARBOHYD     63     63       POTENTIAL.
FT   CARBOHYD     79     79       POTENTIAL.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    139    139       POTENTIAL.
FT   CARBOHYD    372    372       POTENTIAL.
FT   CARBOHYD    392    392       POTENTIAL.
FT   CARBOHYD    421    421       POTENTIAL.
FT   CARBOHYD    738    738       POTENTIAL.
FT   CONFLICT     83     83       Q -> H (IN REF. 1).
FT   CONFLICT    125    125       S -> N (IN REF. 1).
FT   CONFLICT    182    188       FEEIGNE -> LRRLET (IN REF. 1).
FT   CONFLICT    200    200       D -> N (IN REF. 1).
FT   CONFLICT    366    375       TSNVVRNESS -> DFKRGKERKF (IN REF. 1).
FT   CONFLICT    808    818       AKRAFDGQFVK -> QSVLSMGNLTNELTIYSSSHRDIHKT
FT                                FSYLHTMYI (IN REF. 1).
SQ   SEQUENCE   818 AA;  93404 MW;  8D658EBB CRC32;

  Query Match           38.3%;  Score 54;  DB 3;  Length 818;
  Best Local Similarity  33.3%;  Pred. No. 2.01e+00;
  Matches     7;  Conservative    7;  Mismatches   7;  Indels   0;  Gaps   0;

Db    511 ivdfhsrkaekcdkgnvlgks 531
          ::| :: |: || : :| | |
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   13
ID   YR71_CAEEL     STANDARD;      PRT;  1039 AA.
AC   Q09564;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.
GN   F43C1.1.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   JASSAL B.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN
CC       MANY PROTEINS. NUMBER IN THIS PROTEIN: 3.
CC   -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
DR   EMBL; Z46937; G603526; -.
DR   WORMPEP; F43C1.1; CE01582.
KW   HYPOTHETICAL PROTEIN; LEUCINE-REPEAT; REPEAT.
FT   DOMAIN      216    284       LEUCINE-RICH REPEATS.
FT   REPEAT      216    238       LRR 1.
FT   REPEAT      239    261       LRR 2.
FT   REPEAT      262    284       LRR 3.
FT   DOMAIN      669    903       PP2C-LIKE.
SQ   SEQUENCE   1039 AA;  118182 MW;  877F95CB CRC32;

  Query Match           38.3%;  Score 54;  DB 11;  Length 1039;
  Best Local Similarity  38.1%;  Pred. No. 2.01e+00;
  Matches     8;  Conservative    5;  Mismatches   7;  Indels   1;  Gaps   1;

Db    677 vsgsrgmknkqcirqvrvent 697
          |   :| |:  |:|| :|| :
Qy      1 VIDHQGTKSSKCVRQ-KVEGS 20


RESULT   14
ID   E411_ADE05     STANDARD;      PRT;   116 AA.
AC   P04489;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE   PROBABLE EARLY E4 11 KD PROTEIN.
OS   HUMAN ADENOVIRUS TYPE 5.
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83164198.
RA   SARNOW P., HEARING P., ANDERSON C.W., REICH N., LEVINE A.J.;
RL   J. MOL. BIOL. 162:565-583(1982).
RN   [2]
RP   COMPLETE GENOME.
RX   MEDLINE; 92087470.
RA   CHROBOCZEK J., BIEBER F., JACROT B.;
RL   VIROLOGY 186:280-285(1992).
DR   EMBL; M73260; -; NOT_ANNOTATED_CDS.
DR   EMBL; X02998; G58502; -.
DR   PIR; B03807; Q4ADE5.
KW   EARLY PROTEIN.
SQ   SEQUENCE   116 AA;  13298 MW;  66EA9B5C CRC32;

  Query Match           37.6%;  Score 53;  DB 3;  Length 116;
  Best Local Similarity  60.0%;  Pred. No. 3.25e+00;
  Matches     6;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db      3 rclrlkvega 12
          :|:| ||||:
Qy     11 KCVRQKVEGS 20


RESULT   15
ID   E411_ADE02     STANDARD;      PRT;   116 AA.
AC   P03241;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   PROBABLE EARLY E4 11 KD PROTEIN.
OS   HUMAN ADENOVIRUS TYPE 2.
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82059444.
RA   HERISSE J., RIGOLET M., DUPONT DE DINECHIN S., GALIBERT F.;
RL   NUCLEIC ACIDS RES. 9:4023-4042(1981).
DR   EMBL; J01917; G209839; -.
DR   PIR; A03807; Q4ADE2.
KW   EARLY PROTEIN.
SQ   SEQUENCE   116 AA;  13255 MW;  950D6981 CRC32;

  Query Match           37.6%;  Score 53;  DB 3;  Length 116;
  Best Local Similarity  60.0%;  Pred. No. 3.25e+00;
  Matches     6;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db      3 rclrlkvega 12
          :|:| ||||:
Qy     11 KCVRQKVEGS 20


RESULT   16
ID   GRN_MOUSE      STANDARD;      PRT;   589 AA.
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AC   P28798;
DT   01-DEC-1992 (REL. 24, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   GRANULINS PRECURSOR (ACROGRANIN).
GN   GRN.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93245991.
RA   BABA T., NEMOTO H., WATANABE K., ARAI Y., GERTON G.L.;
RL   FEBS LETT. 322:89-94(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 92317004.
RA   PLOWMAN G.D., GREEN I.M., NEUBAUER M.G., BUCKLEY S., MCDONALD V.L.,
RA   TODARO G.I., SHOYAB M.;
RL   J. BIOL. CHEM. 267:13073-13078(1992).
CC   -!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
CC       PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC   -!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
DR   EMBL; D16195; G286068; -.
DR   EMBL; M86736; G191767; -.
DR   EMBL; X62321; G50852; -.
DR   EMBL; S59740; -; NOT_ANNOTATED_CDS.
DR   PROSITE; PS00799; GRANULINS.
KW   CYTOKINE; REPEAT; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1    17       POTENTIAL.
FT   CHAIN        18   589       ACROGRANIN.
FT   PEPTIDE     ?58   ?113      GRANULIN 1.
FT   PEPTIDE    ?122   ?178      GRANULIN 2.
FT   PEPTIDE     205    260      GRANULIN 3.
FT   PEPTIDE     280    334      GRANULIN 4.
FT   PEPTIDE     362   ?414      GRANULIN 5.
FT   PEPTIDE     440   ?493      GRANULIN 6.
FT   PEPTIDE    ?517   ?568      GRANULIN 7.
FT   CARBOHYD     38     38      POTENTIAL.
FT   CARBOHYD    263    263      POTENTIAL.
FT   CARBOHYD    373    373      POTENTIAL.
FT   CARBOHYD    526    526      POTENTIAL.
FT   CONFLICT    350    350      L -> R (IN REF. 2).
SQ   SEQUENCE   589 AA;  63458 MW;  96FD3D02 CRC32;

  Query Match           37.6%;  Score 53;  DB 4;  Length 589;
  Best Local Similarity  35.7%;  Pred. No. 3.25e+00;
  Matches    5;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db    560 hcsargtkclrkki 573
          | :::::||:| |:
Qy      4 HQGTKSSKCVRQKV 17


RESULT   17
ID   GALC_HUMAN     STANDARD;      PRT;   669 AA.
AC   P54803;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE)
DE   (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE)
DE   (GALACTOCEREBROSIDE BETA-GALACTOSIDASE).
GN   GALC.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC.  EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=PLACENTA, AND SKIN FIBROBLAST;
RX   MEDLINE; 94128088.
RA   SAKAI N., INUI K., FUJII N., FUKUSHIMA H., NISHIMOTO J.,
RA   YANAGIHARA I., ISEGAWA Y., IWAMATSU A., OKADA S.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 198:485-491(1994).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-59 AND 436-454.
RC   TISSUE=BRAIN, AND TESTIS;
RX   MEDLINE; 94108435.
RA   CHEN Y.Q., RAFI M.A., DE GALA G., WENGER D.A.;
RL   HUM. MOL. GENET. 2:1841-1845(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95324938.
RA   LUZI P., RAFI M.A., WENGER D.A.;
RL   GENOMICS 26:407-409(1995).
RN   [4]
RP   SEQUENCE OF 27-45; 436-454, AND CHARACTERIZATION.
RC   TISSUE=URINE;
RX   MEDLINE; 94002192.
RA   CHEN Y.Q., WENGER D.A.;
RL   BIOCHIM. BIOPHYS. ACTA 1170:53-61(1993).
RN   [5]
RP   VARIANTS GLD ALA-302 AND GLY-550.
RA   TATSUMI N., INUI K., SAKAI N., FUKUSHIMA H., NISHIMOTO J.,
RA   YANAGIHARA I., NISHIGAKI T., TSUKAMOTO H., FU L., TANIIKE M.,
RA   OKADA S.;
RL   HUM. MOL. GENET. 45:1865-1868(1995).
CC   -!- FUNCTION: HYDROLYSES THE GALACTOSE ESTER BONDS OF
CC       GALACTOSYLCERAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCERAMIDE, AND
CC       MONOGALACTOSYLDIGLYCERIDE. ENZYME WITH VERY LOW ACTIVITY
CC       RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, A
CC       MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
CC       INTESTINE AND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.
CC       ACTIVITY IS LOST WHEN HEATED AT 52 DEGREES CELSIUS FOR FIVE
CC       MINUTES.
CC   -!- CATALYTIC ACTIVITY: D-GALACTOSYL-N-ACYLSPHINGOSINE + H(2)O = D-
CC       GALACTOSE + N-ACYLSPHINGOSINE.
CC   -!- SUBCELLULAR LOCATION: LYSOSOMAL.
CC   -!- TISSUE SPECIFICITY: HIGHEST LEVEL OF ACTIVITY IN TESTES COMPARED
CC       TO BRAIN, KIDNEY, PLACENTA AND LIVER. CAN ALSO BE FOUND IN URINE.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
CC       SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM.
CC   -!- DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
CC       LEUKODISTROPHY (GLD) (OR KRABBE DISEASE), AN AUTOSOMAL RECESSIVE
CC       DISORDER CHARACTERIZED BY HYPERTONICITY, IRRATIBILITY,
CC       INTELLECTUAL DELAY AND REGRESSION WITHIN THE FIRST SIX MONTHS OF
CC       LIFE. THE AVERAGE AGE AT DEATH IS THIRTEEN MONTHS, ALTHOUGHT LATER
CC       ONSET FORMS HAVE BEEN IDENTIFIED. BIOCHEMICALLY GALC DEFICIENCY
CC       RESULTS IN AN ABNORMAL AND/OR INSUFFICIENT PRODUCTION OF MYELIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
DR   EMBL; D25283; G457444; -.
DR   EMBL; D25284; G457446; -.
DR   EMBL; L23116; G431310; -.
DR   EMBL; L38559; G710535; -.
DR   EMBL; L38544; G710535; JOINED.
DR   EMBL; L38545; G710535; JOINED.
DR   EMBL; L38546; G710535; JOINED.
DR   EMBL; L38547; G710535; JOINED.
DR   EMBL; L38548; G710535; JOINED.
DR   EMBL; L38549; G710535; JOINED.
DR   EMBL; L38550; G710535; JOINED.
DR   EMBL; L38551; G710535; JOINED.
DR   EMBL; L38552; G710535; JOINED.
DR   EMBL; L38553; G710535; JOINED.
DR   EMBL; L38555; G710535; JOINED.
DR   EMBL; L38556; G710535; JOINED.
DR   EMBL; L38557; G710535; JOINED.
DR   EMBL; L38558; G710535; JOINED.
DR   MIM; 245200; -.
KW   HYDROLASE; GLYCOSIDASE; GLYCOPROTEIN; SIGNAL; ALTERNATIVE SPLICING;
KW   DISEASE MUTATION.
FT   SIGNAL        1     26
FT   CHAIN        27    669       GALACTOCEREBROSIDASE.
FT   CARBOHYD    127    127       POTENTIAL.
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FT   CARBOHYD    363    363       POTENTIAL.
FT   CARBOHYD    387    387       POTENTIAL.
FT   CARBOHYD    540    540       POTENTIAL.
FT   CARBOHYD    543    543       POTENTIAL.
FT   CARBOHYD    586    586       POTENTIAL.
FT   VARSPLIC    372    392       SHKHSKCIRPFLPYFNVSQQ ->
FT                                VNFCCCYWINSLLYYWKNKI (IN SHORT FORM).
FT   VARSPLIC    393    669       MISSING (IN SHORT FORM).
FT   VARIANT     302    302       P -> A (IN GLD).
FT   VARIANT     550    550       V -> G (IN GLD).
FT   CONFLICT    546    546       I -> T (IN REF. 3).
SQ   SEQUENCE   669 AA;  75147 MW;  9EF9402F CRC32;

  Query Match           37.6%;  Score 53;  DB 4;  Length 669;
  Best Local Similarity  42.9%;  Pred. No. 3.25e+00;
  Matches    6;  Conservative    4;  Mismatches   4;  Indels   0;  Gaps   0;

Db    367 iietmshkhskcir 380
          :|:  : | |||:|
Qy      1 VIDHQGTKSSKCVR 14


RESULT   18
ID   PGDS_HUMAN     STANDARD;      PRT;  1089 AA.
AC   P16234;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR
DE   (EC 2.7.1.112).
GN   PDGFRA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89130149.
RA   MATSUI T., HEIDARAN M., MIKI T., POPESCU N., LA ROCHELLE W.,
RA   KRAUS M., PIERCE J., AARONSON S.;
RL   SCIENCE 243:800-804(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89296915.
RA   CLAESSON-WELSH L., ERIKSSON A., WESTERMARK B., HELDIN C.H.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 86:4917-4921(1989).
CC   -!- FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND
CC       HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR CAN BIND
CC       EITHER PDGF-A OR PDGF-B.
CC   -!- SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC       PROTEIN KINASES.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE
CC       EXTRACELLULAR DOMAIN CONTAINS FIVE IG-FOLD DOMAINS.
DR   EMBL; M21574; G189734; -.
DR   EMBL; M22734; G189726; -.
DR   PIR; A40162; PFHUGA.
DR   MIM; 173490; -.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM.
KW   TYROSINE-PROTEIN KINASE; RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW   TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; IMMUNOGLOBULIN FOLD;
KW   SIGNAL.
FT   SIGNAL        1     23
FT   CHAIN        24   1089       ALPHA PLATELET-DERIVED GROWTH FACTOR
FT                                RECEPTOR.
FT   DOMAIN       24    524       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    525    549       POTENTIAL.
FT   DOMAIN      550   1089       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      593    954       PROTEIN KINASE.
FT   DOMAIN     1041   1087       SER-RICH.
FT   NP_BIND     599    607       ATP (BY SIMILARITY).
FT   BINDING     627    627       ATP (BY SIMILARITY).
FT   ACT_SITE    818    818       BY SIMILARITY.
FT   MOD_RES     849    849       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   CARBOHYD     42     42       POTENTIAL.
FT   CARBOHYD     76     76       POTENTIAL.
FT   CARBOHYD    103    103       POTENTIAL.
FT   CARBOHYD    179    179       POTENTIAL.
FT   CARBOHYD    353    353       POTENTIAL.
FT   CARBOHYD    359    359       POTENTIAL.
FT   CARBOHYD    458    458       POTENTIAL.
FT   CARBOHYD    468    468       POTENTIAL.
SQ   SEQUENCE  1089 AA;  122669 MW;  43E6902A CRC32;

  Query Match           37.6%;  Score 53;  DB 7;  Length 1089;
  Best Local Similarity  38.1%;  Pred. No. 3.25e+00;
  Matches    8;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    421 vddhhgstgggtvrctaegtp 441
          | ||:|: ::  ||   ||::
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   19
ID   ESG2_TRYBB     STANDARD;      PRT;   329 AA.
AC   P04478;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE   VSG EXPRESSION SITE-ASSOCIATED PROTEIN 221A PRECURSOR (ESAG PROTEIN).
OS   TRYPANOSOMA BRUCEI BRUCEI.
OC   EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;
OC   TRYPANOSOMATIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85254917.
RA   CULLY D.F., IP H.S., CROSS G.A.M.;
RL   CELL 42:173-182(1985).
CC   -!- FUNCTION: NOT KNOWN BUT MAY BE RELATED TO ACTIVATION OF THE
CC       VARIANT SURFACE GLYCOPROTEIN GENES.
DR   EMBL; M11452; G162073; -.
DR   PIR; A03395; VMUT21.
KW   SIGNAL.
FT   SIGNAL        1     23
FT   CHAIN        24    329       VSG EXPRESSION SITE-ASSOCIATED PROTEIN
FT                                221A.
FT   CARBOHYD     73     73       POTENTIAL.
FT   CARBOHYD    294    294       POTENTIAL.
FT   CARBOHYD    308    308       POTENTIAL.
SQ   SEQUENCE   329 AA;  36603 MW;  6B9966CE CRC32;

  Query Match           36.9%;  Score 52;  DB 3;  Length 329;
  Best Local Similarity  70.0%;  Pred. No. 5.22e+00;
  Matches    7;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db    176 akcgsqkveg 185
          :||  |||||
Qy     10 SKCVRQKVEG 19


RESULT   20
ID   OCD_AGRT5      STANDARD;      PRT;   354 AA.
AC   P09773;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   ORNITHINE CYCLODEAMINASE (EC 4.3.1.12) (OCD).
GN   OCD.
OS   AGROBACTERIUM TUMEFACIENS.
OG   PLASMID TIC58.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   RHIZOBIACEAE.
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 88185308.
RA   SANS N., SCHINDLER U., SCHROEDER J.;
RL   EUR. J. BIOCHEM. 173:123-130(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94321320.
RA   ZANKER H., LURZ G., LANGRIDGE U., LANGRIDGE P., KREUSCH D.,
RA   SCHROEDER J.;
RL   J. BACTERIOL. 176:4511-4517(1994).
CC   -!- CATALYTIC ACTIVITY: L-ORNITHINE = L-PROLINE + NH(3).
CC   -!- PATHWAY: LAST STEP IN THE TI-PLASMID-CODED PATHWAY FROM NOPALINE
CC       TO PROLINE.
CC   -!- ENZYME REGULATION: ACTIVITY IS SUBJECT TO SUBSTRATE INHIBITION, IS
CC       STIMULATED BY NAD(+) (PRESUMABLY ACTING AS A CATALYTIC COFACTOR)
CC       AND IS REGULATED BY L-ARGININE.
CC   -!- SIMILARITY: REGIONS OF SIMILARITY WITH E.COLI AND P.AERUGINOSA
CC       CARBAMOYLTRANSFERASES.
DR   EMBL; X07435; G39108; -.
DR   EMBL; Z30316; G496538; -.
DR   PIR; S00402; DUAGO.
KW   LYASE; NAD; PLASMID.
FT   DOMAIN      172    207       REGION OF SUBSTRATE-BINDING SITE
FT                                (POTENTIAL).
SQ   SEQUENCE   354 AA;  38984 MW;  6F310E2E CRC32;

  Query Match           36.9%;  Score 52;  DB 7;  Length 354;
  Best Local Similarity  63.6%;  Pred. No. 5.22e+00;
  Matches     7;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db    312 ryvrdrvegss 322
          : ||::|||||
Qy     11 KCVRQKVEGSS 21


RESULT   21
ID   P2X5_RAT       STANDARD;      PRT;   455 AA.
AC   P51578;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   P2X PURINOCEPTOR 5 (ATP RECEPTOR) (P2X5) (PURINERGIC RECEPTOR).
GN   P2RX5.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COELIAC GANGLION;
RX   MEDLINE; 96256686.
RA   COLLO G., KAWASHIMA E., PICH E., NEIDHART S., NORTH R.A.,
RA   SURPRENANT A., BUELL G.N.;
RL   J. NEUROSCI. 16:2495-2507(1996).
CC   -!- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION
CC       CHANNEL.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
DR   EMBL; X92069; E205287; -.
KW   IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; RECEPTOR; GLYCOPROTEIN.
FT   DOMAIN        1     30       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     31     51       1 (POTENTIAL).
FT   DOMAIN       52    341       EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT   TRANSMEM    342    362       2 (POTENTIAL).
FT   DOMAIN      363    455       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     77     77       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
SQ   SEQUENCE   455 AA;  51479 MW;  7EDE74C3 CRC32;

  Query Match           36.9%;  Score 52;  DB 7;  Length 455;
  Best Local Similarity  35.7%;  Pred. No. 5.22e+00;
  Matches     5;  Conservative    6;  Mismatches   3;  Indels   0;  Gaps   0;

Db    141 vvaghglktgrclr 154
          |:  :| |:::|:|
Qy      1 VIDHQGTKSSKCVR 14


RESULT   22
ID   YIF2_YEAST     STANDARD;      PRT;   121 AA.
AC   P40525;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   PROBABLE 60S RIBOSOMAL PROTEIN YIL052C.
GN   YIL052C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA   CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA   GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA   LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA   RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA   WALSH S.V., WHITEHEAD S.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
DR   EMBL; Z38060; G557816; -.
DR   EMBL; Z47047; G763294; -.
DR   PIR; S48427; S48427.
DR   PROSITE; PS01145; RIBOSOMAL_L34E_1.
DR   PROSITE; PS01146; RIBOSOMAL_L34E_2.
KW   HYPOTHETICAL PROTEIN; RIBOSOMAL PROTEIN.
SQ   SEQUENCE   121 AA;  13641 MW;  9CA08085 CRC32;

  Query Match           36.2%;  Score 51;  DB 11;  Length 121;
  Best Local Similarity  25.0%;  Pred. No. 8.32e+00;
  Matches     3;  Conservative    8;  Mismatches   1;  Indels   0;  Gaps   0;

Db     78 gsrcancvkeri 89
          |:: ::||::::
Qy      6 GTKSSKCVRQKV 17


RESULT   23
ID   VP67_NPVGM     STANDARD;      PRT;   337 AA.
AC   P04872;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   MAJOR ENVELOPE GLYCOPROTEIN (GP67) (FRAGMENT).
GN   GP67 OR P67.
OS   GALLERIA MELLONELLA NUCLEAR POLYHEDROSIS VIRUS (GMNPV).
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84132566.
RA   BLINOV V.M., GUTOROV V.V., HOLODILOV N.G., ILJICHEV A.A.,
RA   KARGINOV V.A., MIKRJUKOV N.N., MORDVINOV V.A., NIKONOV I.V.,
RA   PETROV N.A., URMANOV I.H., VASILENKO S.K.;
RL   FEBS LETT. 167:254-258(1984).
CC   -!- FUNCTION: PHOSPHOGLYCOPROTEIN WHICH IS LOCATED ON THE SURFACE OF
CC       BOTH INFECTED CELLS AND BUDDED VIRIONS. IT IS SUGGESTED THAT THE
CC       VIRUS ENTRY INTO CELLS IS PRIMARILY BY THE ENDOCYTIC PATHWAY AND
CC       THAT THIS PROTEIN MAY PLAY A ROLE IN FUSION OF THE VIRAL ENVELOPE
CC       WITH THE ENDOSOMAL MEMBRANE.
CC   -!- PTM: ACYLATED BY A PALMITIC ACID GROUP.
CC   -!- SIMILARITY: TO THE CORRESPONDING PROTEIN IN OTHER BACULOVIRUSES;
CC       ALSO SOME SIMILARITY TO DHORI AND THOGOTO VIRUSES MAJOR ENVELOPE
CC       GLYCOPROTEIN.
CC   -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THIS SEQUENCE WAS
CC       TRANSLATED USING THE ACMNPV SEQUENCE AS A TEMPLATE. THERE IS A
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CC       FRAMESHIFT IN THE ORIGINAL NUCLEOTIDE SEQUENCE.
DR   EMBL; X00410; G58675; ALT_FRAME.
DR   PIR; S07237; S07237.
KW   GLYCOPROTEIN; TRANSMEMBRANE; PHOSPHORYLATION; LIPOPROTEIN.
FT   NON_TER       1      1
FT   CARBOHYD     76     76       POTENTIAL.
FT   CARBOHYD    114    114       POTENTIAL.
FT   CARBOHYD    271    271       POTENTIAL.
FT   CARBOHYD    301    301       POTENTIAL.
FT   NON_TER     337    337
SQ   SEQUENCE   337 AA;  39000 MW;  3772A3FA CRC32;

  Query Match           36.2%;  Score 51;  DB 10;  Length 337;
  Best Local Similarity  45.5%;  Pred. No. 8.32e+00;
  Matches     5;  Conservative    5;  Mismatches   1;  Indels   0;  Gaps   0;

Db    180 kfnrcikrkve 190
          | ::|:::|||
Qy      8 KSSKCVRQKVE 18


RESULT   24
ID   ADH1_ZYMMO     STANDARD;      PRT;   337 AA.
AC   P20368;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   ALCOHOL DEHYDROGENASE I (EC 1.1.1.1) (ADH I).
GN   ADHA.
OS   ZYMOMONAS MOBILIS.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   UNCERTAIN.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CP4;
RX   MEDLINE; 90236908.
RA   KESHAV K.F., YOMANO L.P., AN H., INGRAM L.O.;
RL   J. BACTERIOL. 172:2491-2497(1990).
RN   [2]
RP   SEQUENCE OF 1-40 FROM N.A.
RC   STRAIN=CP4;
RX   MEDLINE; 93308069.
RA   YOMANO L.P., SCOPES R.K., INGRAM L.O.;
RL   J. BACTERIOL. 175:3926-3933(1993).
RN   [3]
RP   SEQUENCE OF 1-31.
RX   MEDLINE; 86108298.
RA   NEALE A.D., SCOPES R.K., KELLY J.M., WETTENHALL R.E.H.;
RL   EUR. J. BIOCHEM. 154:119-124(1986).
CC   -!- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NADH.
CC   -!- PATHWAY: ETHANOLOGENIC.
CC   -!- ENZYME REGULATION: ADHA IS INHIBITED BY ETHANOL.
CC   -!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
CC   -!- SUBUNIT: MULTIMERIC (WITH DIFFERENT RATIOS OF MONOMERS).
CC   -!- IN Z.MOBILIS THERE ARE TWO ISOZYMES OF ALCOHOL DEHYDROGENASE.
CC   -!- SIMILARITY: BELONGS TO THE ZINC ALCOHOL DEHYDROGENASES.
DR   EMBL; M32100; G155571; -.
DR   EMBL; L09650; E84191; -.
DR   PIR; A35260; A35260.
DR   PIR; A24801; A24801.
DR   HSSP; P00325; 1HDX.
DR   PROSITE; PS00059; ADH_ZINC.
KW   OXIDOREDUCTASE; ZINC; NAD.
FT   METAL        37     37       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL        58     58       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL        89     89       ZINC (SECOND ATOM) (BY SIMILARITY).
FT   METAL        92     92       ZINC (SECOND ATOM) (BY SIMILARITY).
FT   METAL        95     95       ZINC (SECOND ATOM) (BY SIMILARITY).
FT   METAL       103    103       ZINC (SECOND ATOM) (BY SIMILARITY).
FT   METAL       145    145       ZINC (CATALYTIC) (BY SIMILARITY).
FT   CONFLICT     17     17       T -> I (IN REF. 3).
FT   CONFLICT     26     26       E -> F (IN REF. 3).
FT   CONFLICT     28     28       L -> H (IN REF. 3).
FT   CONFLICT     30     30       E -> P (IN REF. 3).
SQ   SEQUENCE   337 AA;  36094 MW;  7B77AE15 CRC32;

  Query Match           36.2%;  Score 51;  DB 1;  Length 337;
  Best Local Similarity  30.0%;  Pred. No. 8.32e+00;
  Matches     6;  Conservative    7;  Mismatches   7;  Indels   0;  Gaps   0;

Db    210 vinpknedaakiiqekvgga 229
          ||:     ::| :::|| |:
Qy      1 VIDHQGTKSSKCVRQKVEGS 20


RESULT   25
ID   KPY1_ECOLI     STANDARD;      PRT;   462 AA.
AC   P14178;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PYRUVATE KINASE I (EC 2.7.1.40) (PK-1).
GN   PYKF.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89386643.
RA   OHARA O., DORIT R.L., GILBERT W.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 86:6883-6887(1989).
RN   [2]
RP   SEQUENCE OF 293-319; 369-385 AND 389-404.
RX   MEDLINE; 89228557.
RA   SPERANZA M.L., VALENTINI G., IADAROLA P., STOPPINI M., MALCOVATI M.,
RA   FERRI G.;
RL   BIOL. CHEM. HOPPE-SEYLER 370:211-216(1989).
RN   [3]
RP   SEQUENCE OF 1-48.
RX   MEDLINE; 91315755.
RA   VALENTINI G., STOPPINI M., SPERANZA M.L., MALCOVATI M., FERRI G.;
RL   BIOL. CHEM. HOPPE-SEYLER 372:91-93(1991).
RN   [4]
RP   SEQUENCE OF 1-12.
RC   STRAIN=K12 / EMG2;
RA   LINK A.J.;
RL   SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.
CC   -!- CATALYTIC ACTIVITY: ATP + PYRUVATE = ADP + PHOSPHOENOLPYRUVATE.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
CC   -!- PATHWAY: FINAL STEP IN GLYCOLYSIS.
CC   -!- ENZYME REGULATION: BELONGS TO TYPE I PK; FRUCTOSE
CC       1,6-BISPHOSPHATE-ACTIVATED.
CC   -!- SIMILARITY: HIGH, WITH OTHER PYRUVATE KINASES.
DR   EMBL; M24636; G147276; -.
DR   PIR; S03397; S03397.
DR   PIR; S13434; S13434.
DR   PIR; S29004; S29004.
DR   HSSP; P11974; 1PKN.
DR   ECO2DBASE; G054.7; 6TH EDITION.
DR   ECOGENE; EG10804; PYKF.
DR   PROSITE; PS00110; PYRUVATE_KINASE.
KW   TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; MAGNESIUM.
FT   ACT_SITE    220    220       BY SIMILARITY.
FT   METAL       222    222       MAGNESIUM (BY SIMILARITY).
FT   METAL       243    243       MAGNESIUM (BY SIMILARITY).
FT   METAL       244    244       MAGNESIUM (BY SIMILARITY).
FT   CONFLICT     44     44       G -> S (IN REF. 3).
FT   CONFLICT    379    379       Q -> N (IN REF. 2).
FT   CONFLICT    401    401       T -> D (IN REF. 2).
SQ   SEQUENCE   462 AA;  50308 MW;  D83D4CE0 CRC32;

  Query Match           36.2%;  Score 51;  DB 5;  Length 462;
  Best Local Similarity  50.0%;  Pred. No. 8.32e+00;
  Matches     7;  Conservative    3;  Mismatches   4;  Indels   0;  Gaps   0;
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Db    375 vvatqggksaravr 388
          |:  || ||:: ||
Qy      1 VIDHQGTKSSKCVR 14
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Search completed: Tue Jul 29 07:31:16 1997
Job time : 17 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 29 07:32:27 1997; MasPar time 2.20 Seconds
104.214 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHQGTKSSKCVRQKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 18.695; Variance 55.381; scale 0.338

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	141	100.0	21	15	R77605	Pro-C5 polypeptide KS	8.75e-10
2	141	100.0	1676	15	R77604	Pro-C5 polypeptide.	8.75e-10
3	55	39.0	264	4	R22271	CSHase.	2.91e+01
4	54	38.3	1732	17	R96029	P. gingivalis porphyp	3.72e+01
5	54	38.3	3163	16	R94347	Hepatitis GB virus (H	3.72e+01
6	53	37.6	589	3	R14327	Mouse epithelin precu	4.75e+01
7	53	37.6	652	15	R88124	Tobacco mosaic virus	4.75e+01
8	53	37.6	1009	5	R26206	Type B human platelet	4.75e+01
9	53	37.6	1089	2	R06910	Alpha type PDGF recep	4.75e+01
10	53	37.6	1089	2	R08267	Platelet derived grow	4.75e+01
11	53	37.6	1196	19	W04326	Rat petrin.	4.75e+01
12	52	36.9	354	6	R33439	Ornithine cyclodeamin	6.06e+01
13	51	36.2	589	3	R14325	Rat epithelin precurs	7.71e+01
14	51	36.2	914	3	R15785	B.thuringiensis toxin	7.71e+01
15	51	36.2	956	3	R15784	B.thuringiensis toxin	7.71e+01
16	51	36.2	986	9	R25141	JAK2.	7.71e+01
17	51	36.2	1100	3	R15783	B.thuringiensis toxin	7.71e+01
18	51	36.2	1129	13	R70830	Murine JAK2 kinase.	7.71e+01
19	51	36.2	1144	15	R88123	Tobacco mosaic virus	7.71e+01
20	51	36.2	1144	15	R88122	Tobacco mosaic virus	7.71e+01
21	51	36.2	1588	9	R46605	Malarial PfEMP3 epito	7.71e+01
22	51	36.2	1663	9	R46608	Plasmodium falciparum	7.71e+01
23	49	34.8	429	10	R50036	Hantaian virus Nucleo	1.24e+02
24	49	34.8	487	3	R13794	Drosophila hormone re	1.24e+02
25	49	34.8	694	1	R04107	DNA-binding protein G	1.24e+02
26	49	34.8	1323	10	R55248	N-methyl-D-aspartic a	1.24e+02
27	49	34.8	1336	12	R66041	Human N-methyl-D-aspa	1.24e+02
28	49	34.8	3080	1	P93285	Sequence of clone HIV	1.24e+02
29	48	34.0	399	19	W04218	Human urinary bladder	1.58e+02
30	48	34.0	925	14	R79148	Human insulin recepto	1.58e+02
31	48	34.0	1299	15	R86304	Drosophila patched pr	1.58e+02
32	47	33.3	122	16	R81443	Hepatitis GB virus (H	1.99e+02
33	47	33.3	458	3	R15149	CD4 coordinate system	1.99e+02
34	47	33.3	498	3	R12255	HIV-1 strain OYI GAG	1.99e+02
35	47	33.3	792	16	R85198	Avenacinase - a sapon	1.99e+02
36	47	33.3	793	16	R85200	Avenacinase-like prot	1.99e+02
37	47	33.3	793	16	R85199	Avenacinase-like prot	1.99e+02
38	47	33.3	2873	17	R87559	Hepatitis virus clone	1.99e+02
39	47	33.3	2873	18	R90796	HGV-PNF 2161 polyprot	1.99e+02
40	46	32.6	376	5	R25429	Cellulase contained i	2.51e+02
41	46	32.6	376	7	R37151	Dye transfer inhibiti	2.51e+02
42	46	32.6	376	5	R27969	Endoglucanase enzyme.	2.51e+02
43	46	32.6	376	5	R25527	Fusarium oxysporum DS	2.51e+02
44	46	32.6	376	3	R15272	Fusarium oxysporum DS	2.51e+02
45	46	32.6	376	5	R25466	Endoglucanase #2.	2.51e+02
46	46	32.6	376	8	R42064	Endoglucanase enzyme.	2.51e+02
47	46	32.6	1087	17	R96028	P. gingivalis haemagg	2.51e+02
48	46	32.6	1232	19	R98217	Neuronal apoptosis in	2.51e+02
49	46	32.6	1358	17	R96032	P. gingivalis hagD ha	2.51e+02
50	46	32.6	1687	17	R96033	P. gingivalis haemagg	2.51e+02
51	46	32.6	1704	13	R70188	Arg-gingipain-2 prepo	2.51e+02
52	45	31.9	33	16	R82896	Human B7-1 signal pep	3.16e+02
53	45	31.9	51	8	R38884	lac peptide fragment.	3.16e+02
54	45	31.9	170	3	R10845	Feline interferon fro	3.16e+02
55	45	31.9	171	1	P90398	Feline interferon	3.16e+02
56	45	31.9	194	1	P90399	Feline interferon	3.16e+02
57	45	31.9	288	13	R67989	Human B lymphocyte an	3.16e+02
58	45	31.9	312	4	R21848	Sequence of Plasmodiu	3.16e+02
59	45	31.9	360	16	R86552	Mutant lactose repres	3.16e+02
60	45	31.9	360	8	R40926	Wild-type lacI.	3.16e+02
61	45	31.9	370	8	R40927	CpG depleted lacI gen	3.16e+02
62	45	31.9	386	12	R60549	Murine developmental	3.16e+02
63	45	31.9	505	14	R77172	Condensing enzyme clo	3.16e+02
64	45	31.9	605	14	R74186	Chick p78.	3.16e+02
65	45	31.9	709	1	P91934	B1 antigen.	3.16e+02
66	45	31.9	845	13	R70065	Hepatitis B virus pol	3.16e+02
67	45	31.9	850	11	R60546	Mature murine develop	3.16e+02
68	45	31.9	868	2	R07454	Second open reading f	3.16e+02
69	45	31.9	874	11	R60545	Murine developmental	3.16e+02
70	45	31.9	880	13	R77846	Mouse Rse rPTK.	3.16e+02
71	45	31.9	1277	10	R52701	Plasmid pASK60-Strep	3.16e+02
72	45	31.9	2324	1	R05707	Acetyl-CoA-carboxylas	3.16e+02
73	45	31.9	2910	17	R87566	Hepatitis G virus clo	3.16e+02
74	45	31.9	2910	18	R90797	HGV-JC variant polypr	3.16e+02
75	45	31.9	2938	11	R59923	GAP protein Iral.	3.16e+02
76	45	31.9	3011	16	R95020	Hepatitis GB virus (H	3.16e+02
77	44	31.2	15	1	P90197	Antigenic peptide for	3.97e+02
78	44	31.2	20	12	R68766	Cytotoxic T lymphocyt	3.97e+02
79	44	31.2	23	1	P80572	Peptide region of hum	3.97e+02
80	44	31.2	25	12	R68764	Cytotoxic T lymphocyt	3.97e+02
81	44	31.2	35	12	R63489	Human MR77 serotonin	3.97e+02
82	44	31.2	130	1	P91387	HIV LTR sequence	3.97e+02
83	44	31.2	130	10	R56876	N-terminal fragment e	3.97e+02
84	44	31.2	168	10	R55858	HIV-1 MA delta-116-12	3.97e+02
85	44	31.2	355	7	R38297	dTDP-D-glucose syntha	3.97e+02
86	44	31.2	422	11	R58599	Fowlpox virus protein	3.97e+02
87	44	31.2	500	2	P70269	The sequence encoding	3.97e+02
88	44	31.2	504	4	P93707	Sequence of the gag p	3.97e+02
89	44	31.2	508	2	P70666	Sequence encoded by L	3.97e+02
90	44	31.2	512	8	R43866	HTLV-III GAG gene pro	3.97e+02
91	44	31.2	515	1	P91235	(ENV-80)(GAG-VII)(Hex	3.97e+02
92	44	31.2	528	13	R73006	Aminopeptidase O12 cl	3.97e+02
93	44	31.2	529	14	R74188	Mouse p78.	3.97e+02

94	44	31.2	533	3	R15057	Cytochrome P450C25.	3.97e+02
95	44	31.2	600	2	P70541	HTLV-III gag/env gene	3.97e+02
96	44	31.2	600	2	P70544	Sequence of HTLV-III	3.97e+02
97	44	31.2	741	1	P80136	Neisseria IgA-Proteas	3.97e+02
98	44	31.2	1025	8	R38863	GC-B.	3.97e+02
99	44	31.2	1047	3	R10399	Human Natriuretic Pep	3.97e+02
100	44	31.2	1047	3	R10867	NPRB(Pro655, Glu656,	3.97e+02

ALIGNMENTS

```
RESULT    1
ID   R77605 standard; Protein; 21 AA.
AC   R77605;
DT   02-APR-1996  (first entry)
DE   Pro-C5 polypeptide KSSKC epitope.
KW   Complement C5; haemolysis; kidney; glomerulonephritis;
KW   monoclonal antibody; antiinflammatory; antibody engineering;
KW   humanised antibody; KSSKC epitope.
OS   Homo sapiens.
PN   WO9529697-A1.
PD   09-NOV-1995.
PF   01-MAY-1995; U05688.
PR   02-MAY-1994; US-236208.
PA   (ALEX-) ALEXION PHARM INC.
PI   Evans MJ,  Matis L,  Mueller EE,  Nye SH,  Rollins S;
PI   Rother RP,  Springhorn J P,  Squinto SP,  Thomas TC;
PI   Wang Y,  Wilkins JA;
DR   WPI; 95-392923/50.
PT   Treating glomerulonephritis with antibody against complement C5
PT   component  - to inhibit complement induced cell lysis
PS   Example 13; Page 81; 181pp; English.
CC   The cDNA sequence of the complement C5 gene transcript predicts a
CC   secreted pro-C5 precursor of 1676 amino acids (R77604).  C5 is a
CC   beta-globulin heterodimer thought to play a role in the pathogenesis
CC   of glomerulonephritis (GN).  Cleavage of the C5 alpha-chain
CC   by a convertase enzyme generates anaphylatoxic C5a.  Monoclonal
CC   and humanised recombinant antibodies that recognise the alpha-chain
CC   KSSKC epitope (R77605) block C5a generation, thereby reducing
CC   glomerular inflammation and kidney dysfunction associated with GN.
SQ   Sequence   21 AA;

  Query Match          100.0%;  Score 141;  DB 15;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 8.75e-10;
  Matches    21;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 vidhqgtksskcvrqkvegss 21
          |||||||||||||||||||||
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT    2
ID   R77604 standard; Protein; 1676 AA.
AC   R77604;
DT   15-MAR-1996  (first entry)
DE   Pro-C5 polypeptide.
KW   Complement C5; haemolysis; kidney; glomerulonephritis;
KW   monoclonal antibody; antiinflammatory; antibody engineering;
KW   humanised antibody.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT   /label= Sig_peptide
FT   Protein         19..673
FT   /label= Beta-chain
FT   Cleavage_site   673..674
FT   Cleavage_site   677..678
FT   Peptide         674..677
FT   label= Cleavage_peptide
FT   Protein         678..1676
FT   /label= Alpha-chain
FT   /note= "amino acids 872-892 (854-874 of
FT   the mature protein) comprise the KSSKS
FT   epitope"
FT   Peptide         678..751
FT   /label= C5a
FT   Cleavage_site   751..752
FT   /label= Convertase_cleavage_site
FT   Modified_site   911
FT   /label= N-glycosylation_site
FT   Modified_site   1115
FT   /label= N-glycosylation_site
FT   Modified_site   1630
FT   /label= N-glycosylation_site
PN   WO9529697-A1.
PD   09-NOV-1995.
PF   01-MAY-1995; U05688.
PR   02-MAY-1994; US-236208.
PA   (ALEX-) ALEXION PHARM INC.
PI   Evans MJ,  Matis L,  Mueller EE,  Nye SH,  Rollins S;
PI   Rother RP,  Springhorn J P,  Squinto SP,  Thomas TC;
PI   Wang Y,  Wilkins JA;
DR   WPI; 95-392923/50.
PT   Treating glomerulonephritis with antibody against complement C5
PT   component  - to inhibit complement induced cell lysis
PS   Example 13; Page 82-92; 181pp; English.
CC   The cDNA sequence of the complement C5 gene transcript predicts a
CC   secreted pro-C5 precursor of 1676 amino acids (R77604).  C5 is a
CC   beta-globulin heterodimer thought to play a role in the pathogenesis
CC   of glomerulonephritis (GN).  Cleavage of the C5 alpha-chain
CC   by a convertase enzyme generates anaphylatoxic C5a.  Monoclonal
CC   and humanised recombinant antibodies that recognise the alpha-chain
CC   KSSKC epitope (R77605) block C5a generation, thereby reducing
CC   glomerular inflammation and kidney dysfunction associated with GN.
SQ   Sequence   1676 AA;

  Query Match          100.0%;  Score 141;  DB 15;  Length 1676;
  Best Local Similarity 100.0%;  Pred. No. 8.75e-10;
  Matches    21;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    872 vidhqgtksskcvrqkvegss 892
          |||||||||||||||||||||
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT    3
ID   R22271 standard; Protein; 264 AA.
AC   R22271;
DT   30-JUL-1992  (first entry)
DE   CSHase.
KW   N-carbamoyl-sarcosine amidohydrolase; CSH; assay; diagnosis;
KW   creatinine.
OS   Arthrobacter sp. DSM 2563.
PN   EP-476670-A.
PD   25-MAR-1992.
PF   19-SEP-1991; 115974.
PR   20-SEP-1990; DE-029844.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PI   Burtscher H, Schumacher G;
DR   WPI; 92-098378/13.
DR   N-PSDB; Q22713.
PT   Recombinant DNA encoding N-carbamoyl-sarcosine-amidohydrolase -
PT   useful in clinical assay of creatinine, and vectors providing
PT   efficient expression in E.coli
PS   Claim 9; Page 9 + 7; 12pp; German.
CC   The sequence encoding CSHase is useful in assay of creatinine
CC   (for diagnosis of kidney disease).  It can now be prepd. more
CC   simply than by known methods which involve culture of Arthrobacter
CC   on complex media.
SQ   Sequence   264 AA;

  Query Match           39.0%;  Score 55;  DB 4;  Length 264;
  Best Local Similarity 46.2%;  Pred. No. 2.91e+01;
  Matches     6;  Conservative    4;  Mismatches   3;  Indels   0;  Gaps   0;

Db    171 gataagcvrhtve 183
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          |: :: |||: ||
Qy      6 GTKSSKCVRQKVE 18


RESULT    4
ID   R96029 standard; Protein; 1732 AA.
AC   R96029;
DT   04-SEP-1996  (first entry)
DE   P. gingivalis porphypain.
KW   Porphypain; haemagglutinin; periodontal disease; vaccine; antibody.
OS   Porphyromonas gingivalis strain W12.
FH   Key             Location/Qualifiers
FT   Region          688..708
FT   /note= "Pro-Asn repeat region type 1"
FT   Region          887..952
FT   /note= "Pro-Asn repeat region type 2"
FT   Region          946..967
FT   /note= "Pro-Asn repeat region type 1"
FT   Region          985..1006
FT   /note= "Pro-Asn repeat region type 3"
FT   Region          1041..1100
FT   /note= "Pro-Asn repeat region type 4"
FT   Region          1341..1405
FT   /note= "Pro-Asn repeat region type 2"
FT   Region          1430..1451
FT   /note= "Pro-Asn repeat region type 3"
FT   Region          1488..1547
FT   /note= "Pro-Asn repeat region type 4"
FT   Region          1607..1650
FT   /note= "Pro-Asn repeat region type 2"
PN   WO9617936-A2.
PD   13-JUN-1996.
PF   11-DEC-1995; U16108.
PR   09-DEC-1994; US-353485.
PA   (UABR-) UAB RES FOUND.
PA   (UYFL ) UNIV FLORIDA.
PI   Han N,  Lantz M,  Lepine G,  Patti JM,  Progulske-Fox A;
PI   Tumwasorn S;
DR   WPI; 96-287181/29.
DR   N-PSDB; T30653.
PT   Porphyromonas gingivalis genes and proteins - used in the detection
PT   and vaccination against periodontal disease
PS   Claim 5; Page 76-81; 153pp; English.
CC   P. gingivalis W12 cysteine protease, porphypain (R96029), was
CC   identified as the product of the prtP gene (T30653) isolated from
CC   P. gingivalis W12 genomic DNA.  The porphypain shows homology to
CC   the haemagglutinins (see also R96026-28 and R96030-33) of P.
CC   gingivalis 318.  It can be obtd. from transformed host cells and
CC   used as a vaccine to protect humans or animals against periodontal
CC   disease.  Expression in Salmonella cells allows prodn. of a live
CC   vaccine.  The porphypain and haemagglutinins can also be used to
CC   detect the presence of anti-P. gingivalis antibodies and to raise
CC   monoclonal antibodies for diagnostic appln.
SQ   Sequence   1732 AA;

  Query Match           38.3%;  Score 54;  DB 17;  Length 1732;
  Best Local Similarity  31.6%;  Pred. No. 3.72e+01;
  Matches    6;  Conservative    7;  Mismatches   6;  Indels   0;  Gaps   0;

Db   1097 itakgvrspkairgriqgt 1115
          |   | :|:| :| :::|:
Qy      2 IDHQGTKSSKCVRQKVEGS 20


RESULT    5
ID   R94347 standard; Protein; 3163 AA.
AC   R94347;
DT   02-JUL-1996  (first entry)
DE   Hepatitis GB virus (HGBV) clone GB contig A protein prod.
KW   Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
KW   reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A;
KW   tamarin; infected plasma; lambda phage; cDNA library.
OS   Hepatitis GB virus.
FH   Key             Location/Qualifiers
FT   Misc_difference 1..3163
FT   /note= "others correspond to degenerate or STOP
FT   codons in T00129"
PN   WO9521922-A2.
PD   17-AUG-1995.
PF   14-FEB-1995; U02118.
PR   14-FEB-1994; US-196030.
PR   13-MAY-1994; US-242654.
PR   29-JUL-1994; US-283314.
PR   23-NOV-1994; US-344190.
PR   23-NOV-1994; US-344185.
PR   27-JAN-1995; US-344557.
PA   (ABBO ) ABBOTT LAB.
PI   Buijk SL,  Dawson GJ,  Desai SM,  Erker JC,  Leary TP;
PI   Muerhoff AS,  Mushahwar IK,  Pilot-Matias TJ,  Schlauder GG;
PI   Simons JN;
DR   WPI; 95-293123/38.
DR   N-PSDB; T00129.
PT   Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful
PT   for diagnosis and therapy of hepatitis GB virus
PS   Example 9; Pages 401-414; 661pp; English.
CC   Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV
CC   infected tamarin plasma, using standard procedures, was used to
CC   prepare a lambda phage HGBV cDNA library. Clones were rescued
CC   from the lambda phage, searched against a sequence database and
CC   found to be unique HGBV sequences. The clones were then used to
CC   assemble the sequences T00129/30 (GB contig A and B) which encode
CC   the proteins R94345-47 (the 3 possible coding strand reading
CC   frames) and R82072, respectively. Reagents which comprise the HGBV
CC   DNA, or its protein prods. can be used for the diagnosis, therapy
CC   or in a vaccine to prevent HGBV infection.
SQ   Sequence   3163 AA;

  Query Match           38.3%;  Score 54;  DB 16;  Length 3163;
  Best Local Similarity  40.0%;  Pred. No. 3.72e+01;
  Matches    6;  Conservative    5;  Mismatches   4;  Indels   0;  Gaps   0;

Db    528 vvdqrplkcgscvrd 542
          |:|::  | : |||:
Qy      1 VIDHQGTKSSKCVRQ 15


RESULT    6
ID   R14327 standard; Protein; 589 AA.
AC   R14327;
DT   17-JAN-1992  (first entry)
DE   Mouse epithelin precursor.
KW   ET; growth regulation; inhibition; stimulation.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Protein         1..589
FT   /label= precursor
FT   /note= "claim 21, page 55"
FT   Protein         280..335
FT   /label= EP-1
FT   /note= "claim 22, page 55"
FT   Protein         205..261
FT   /label= EP-2
FT   /note= "claim 23, page 55"
FT   Peptide         59..114
FT   /label= EP
FT   /note= "claim 24, page 55"
FT   Peptide         123..179
FT   /label= EP
FT   /note= "claim 25, page 55"
FT   Peptide         362..416
FT   /label= EP
FT   /note= "claim 26, page 56"
FT   Peptide         440..495
FT   /label= EP
FT   /note= "claim 27, page 56"
FT   Peptide         515..570
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FT   /label= EP
FT   /note= "claim 28, page 56"
PN   WO9115510-A.
PD   17-OCT-1991.
PF   03-APR-1991; U02321.
PR   03-APR-1990; US-504508.
PR   13-MAR-1991; US-083796.
PA   (BRIM ) BRISTOL-MYERS SQUIB.
PI   Shoyab M, Plowman GD;
DR   WPI; 91-325168/44.
DR   N-PSDB; Q14340.
PT   New cysteine-rich growth modulating proteins, epithelins - useful
PT   as inhibitors of neoplastic cell growth and to promote wound
PT   healing and treat psoriasis
PS   Disclosure; Fig 23; 97pp; English.
CC   ET-1 is a bifunctional growth regulator, capable of stimulating
CC   the growth of some cell types while inhibiting the growth of others.
CC   ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
CC   bioactivity.  In contrast, however, ET-2 is apparently not capable of
CC   eliciting the growth stimulatory activity characteristic of ET-1 and,
CC   in fact, antagonises this ET-1 activity.
CC   See also Q14338-40, Q14952-53, R14328-9 and R15315-20.
SQ   Sequence   589 AA;

  Query Match           37.6%;  Score 53;  DB 3;  Length 589;
  Best Local Similarity  35.7%;  Pred. No. 4.75e+01;
  Matches    5;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db    560 hcsargtkclrkki 573
          | :::::||:| |:
Qy      4 HQGTKSSKCVRQKV 17


RESULT    7
ID   R88124 standard; Protein; 652 AA.
AC   R88124;
DT   28-MAR-1996  (first entry)
DE   Tobacco mosaic virus resistance N gene truncated protein.
KW   Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
KW   crop improvement; transgenic plant; crop improvement.
OS   Nicotiana glutinosa.
PN   WO9535024-A1.
PD   28-DEC-1995.
PF   16-JUN-1995; U07754.
PR   17-JUN-1994; US-261663.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USDA ) US SEC OF AGRIC.
PI   Baker BJ,  Whitham SA;
DR   WPI; 96-058144/06.
DR   N-PSDB; T09342.
PT   Plant virus resistance gene N sequences from tobacco - useful for
PT   generating transgenic Solanaceous plants resistant to Tobacco Mosaic
PT   Virus
PS   Claim 28; Page 75-79; 98pp; English.
CC   The Nicotiana glutinosa N gene truncated protein (R88124) mediates
CC   resistance to tobacco mosaic virus (TMV).  A cDNA clone (T09342)
CC   coding for the protein was obtd. from a N. glutinosa leaf cDNA
CC   library by transposon tagging.  DNA sequences encoding the
CC   protein can be used to generate transgenic plants, esp. Solanaceae,
CC   resistant to TMV.
SQ   Sequence   652 AA;

  Query Match           37.6%;  Score 53;  DB 15;  Length 652;
  Best Local Similarity  31.3%;  Pred. No. 4.75e+01;
  Matches    5;  Conservative    5;  Mismatches   6;  Indels   0;  Gaps   0;

Db    156 dnrdktdadcirqivd 171
          |::    : |:|| |:
Qy      3 DHQGTKSSKCVRQKVE 18


RESULT    8
ID   R26206 standard; Protein; 1009 AA.
AC   R26206;
DT   09-FEB-1993  (first entry)
DE   Type B human platelet-derived growth factor receptor.
KW   PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT   /label= Signal_peptide
FT   Protein         24..1009
FT   /label= Mature_PDGF-A
PN   WO9213867-A.
PD   20-AUG-1992.
PF   28-JAN-1992; U00730.
PR   31-JAN-1991; US-650793.
PA   (CORT-) COR THERAPEUTICS INC.
PI   Escobedo JA, Fretto LJ, Giese NA, Tomlinson JE, Williams LT;
PI   Wolf D;
DR   WPI; 92-299970/36.
DR   N-PSDB; Q27451.
PT   Platelet derived growth factor receptor (PDGF-R) poly:peptide(s)
PT   - useful as therapeutic and diagnostic agents e.g. for assaying
PT   PDGF activity in sample
PS   Disclosure; Page 90; 109pp; English.
CC   The sequence given is one allele of type A human platelet-derived
CC   growth factor (PDGF) receptor (PDGF-R).  This receptor is typically
CC   found on cells of mesenchymal origin.  It acts while in the form of
CC   two transmembrane glycoproteins, each of which is about 180 kD.
CC   This receptor has three major regions.  The first is a transmembrane
CC   region, which spans the membrane once, separating the regions of the
CC   receptor exterior to the cell from those interior to the cell.  The
CC   second region is an extracellular region which contains the domains
CC   which bind the PDGF.  The third region is an intracellular region
CC   which posseses a tyrosine kinase activity.  This tyrosine kinase
CC   domain is notable in having an insert of approx. 100 amino acids,
CC   as compared with most other receptor tyrosine kinase domains which
CC   are contiguous or have shorter insert sequences.  Fragments of this
CC   sequence between 8 and 400 amino acids comprising one or more PDGF
CC   ligand binding region from the extracellular domain may be used to
CC   bind a PDGF ligand.
SQ   Sequence   1009 AA;

  Query Match           37.6%;  Score 53;  DB 5;  Length 1009;
  Best Local Similarity  38.1%;  Pred. No. 4.75e+01;
  Matches    8;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    381 vddhhgstgggtvrctaegtp 401
          | ||:|: ::  ||   ||::
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT    9
ID   R06910 standard; protein; 1089 AA.
AC   R06910;
DT   16-JAN-1991  (first entry)
DE   Alpha type PDGF receptor deduced from TR4 cDNA clone.
KW   Platelet derived growth factor; T11.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Domain          1..23
FT   /label=signal peptide
FT   Domain          24..524
FT   /label=ligand binding domain
FT   Domain          525..548
FT   /label=transmembrane region
FT   Domain          549..599
FT   /label=juxtamembrane domain
FT   Binding-site    600..627
FT   /label=ATP binding site
FT   Modified-site   849
FT   /label=tyrosine autophosphorylation site
FT   Modified-site   42..44
FT   /label=N-glycos_site
FT   Modified-site   76..78
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FT   /label=N-glycos_site
FT   Modified-site   103..105
FT   /label=N-glycos_site
FT   Modified-site   179..181
FT   /label=N-glycos_site
FT   Modified-site   353..355
FT   /label=N-glycos_site
FT   Modified-site   359..361
FT   /label=N-glycos_site
FT   Modified-site   458..460
FT   /label=N-glycos_site
FT   Modified-site   468..470
FT   /label=N-glycos_site
PN   WO9010013-A.
PD   07-SEP-1990.
PF   08-FEB-1990; U00617.
PR   09-FEB-1989; US-308282.
PA   (USDC ) US SEC OF COMMERCE.
PI   Matsui T, Aaronson SA, Pierce JH;
DR   WPI; 90-290306/38.
DR   N-PSDB; Q05989.
PT   Type alpha platelet-derived growth factor receptor gene - useful
PT   for transforming cells to express novel protein receptor and also
PT   susceptible to genetic engineering.
PS   Claim 7; Fig 3; 64pp; English.
CC   The TR4 clone is the largest cDNA clone related to the T11 genomic
CC   clone, isolated from a library prepd. from human thymus DNA.  The
CC   T4 cDNA clone was isolated from a M426 human embryo fibroblast
CC   cDNA library.   The coding region can be introduced into the pSV2
CC   gpt vector with a simian sarcoma virus LTR as a promoter and
CC   expressed in a host.   The resulting protein is a novel PDGF
CC   receptor designated type alpha (the known receptor is designated
CC   type beta). The polypeptide has a calculated molecular mass of 120
CC   kD and has all the characteristics of a membrane spanning tyrosine
CC   kinase receptor.  The extracellular region comprises a hydrophobic
CC   signal peptide and a ligand binding domain which has structural
CC   homology with the PDGF-R/CSF1-R subfamily.  Ten Cys residues are
CC   spaced at the same positions as in other receptors of the sub-
CC   family and eight potential N-linked glycosylation sites are also
CC   present.  A hydrophobic segment spans the membrane and the cyto-
CC   plasmic region comprises a juxtamembrane region, a tyrosine kinase
CC   region split into TK1 and TK2 by a hydrophilic interkinase region
CC   and a hydrophilic C-terminal tail.  The TK region includes the
CC   consensus ATP binding sequence (G-X-G-X-X-G...K) and a tyrosine
CC   autophosphorylation site homologous to that of pp60(v-src).
SQ   Sequence   1089 AA;

  Query Match           37.6%;  Score 53;  DB 2;  Length 1089;
  Best Local Similarity  38.1%;  Pred. No. 4.75e+01;
  Matches    8;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    421 vddhhgstgggtvrctaegtp 441
          | ||:|: ::  ||   ||::
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   10
ID   R08267 standard; protein; 1089 AA.
AC   R08267;
DT   07-MAR-1991  (first entry)
DE   Platelet derived growth factor (PDGF) receptor protein.
KW   Atherosclerosis; fibrotic diseases.
OS   Homo sapiens.
PN   WO9014425-A.
PD   29-NOV-1990.
PF   21-MAY-1990; U02849.
PR   22-MAY-1989; US-355018.
PA   (ZYMO-) ZYMOGENETICS INC.
PI   Kelly JD, Murray MJ;
DR   WPI; 90-375992/50.
DR   N-PSDB; Q06869.
PT   DNA encoding platelet-derived growth factor - used to transform
PT   cells for culturing to detect PDG agonists and antagonists
PS   Claim 1; Fig 1; 30pp; English.
CC   Gene product may be expressed from a transformed cell. It has
CC   utility in dection of PDGF agonist and antagonist analogues, binding
CC   AA, AB and BB isoforms. PDGF agonists may be used to enhance wound
CC   healing, and antagonists may be used to block the effects of PDGF
CC   eg. in treatment of atherosclerosis or fibrotic diseases.
SQ   Sequence   1089 AA;

  Query Match           37.6%;  Score 53;  DB 2;  Length 1089;
  Best Local Similarity  38.1%;  Pred. No. 4.75e+01;
  Matches    8;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    421 vddhhgstgggtvrctaegtp 441
          | ||:|: ::  ||   ||::
Qy      1 VIDHQGTKSSKCVRQKVEGSS 21


RESULT   11
ID   W04326 standard; Protein; 1196 AA.
AC   W04326;
DT   16-JAN-1997  (first entry)
DE   Rat petrin.
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration.
OS   Rattus sp.
FH   Key             Location/Qualifiers
FT   Misc_difference 129
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 192
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 205
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 219
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 225
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 234
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 243
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 269
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 285
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 312
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 319
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 344
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 358
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 378
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 386
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 465
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 473
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 473
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 494
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 555
FT   /note= "corresponds to stop coodn in DNA sequence"
FT   Misc_difference 593
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 602
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 609
FT   /note= "corresponds to stop codon in DNA sequence"
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FT   Misc_difference 621
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 724
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 736
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 739
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 786
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 841
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 924
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 934
FT   /note= "corresponds to stop coodn in DNA sequence"
FT   Misc_difference 1017
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 1054
FT   /note= "corresponds to stop coodn in DNA sequence"
FT   Misc_difference 1127
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 1147
FT   /note= "corresponds to stop codon in DNA sequence"
FT   Misc_difference 1178
FT   /note= "corresponds to stop codon in DNA sequence"
PN   WO9632476-A1.
PD   17-OCT-1996.
PF   12-APR-1996; CA0214.
PR   13-APR-1995; US-421701.
PA   (MOUN ) MOUNT SINAI HOSPITAL CORP.
PI   Labes M,  Lozano A,  Roach A,  Roder J;
DR   WPI; 96-477127/47.
DR   N-PSDB; T38484.
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
PS   Claim 9; Page 57-61; 119pp; English.
CC   Rat petrin (W04326) is a protein involved in modulating neurite
CC   growth inhibition.  The amino sequence was deduced from a cDNA
CC   clone (T38484) derived from an adult rat brain cDNA library; no
CC   coding sequence was indicated.  Petrin is a new member of the
CC   protein phosphatase 2C family, and is expressed in neurons in brain
CC   tissue, partic. in the Purkinje cells of the cerebellum.  Petrin,
CC   and antibodies raised against it, can be used to modulate neurite
CC   growth and axonal regeneration.
SQ   Sequence   1196 AA;

  Query Match           37.6%;  Score 53;  DB 19;  Length 1196;
  Best Local Similarity  61.5%;  Pred. No. 4.75e+01;
  Matches    8;  Conservative    1;  Mismatches   4;  Indels   0;  Gaps   0;

Db    900 vpshsgtksphcv 912
          |  | ||||: ||
Qy      1 VIDHQGTKSSKCV 13


RESULT   12
ID   R33439 standard; Protein; 354 AA.
AC   R33439;
DT   06-JUL-1993  (first entry)
DE   Ornithine cyclodeaminase C58 from Ti plasmid pTiC58
KW   mu-crystallins; drug targetting; nervous acting drugs; CNS; neural;
KW   neuronal; neurotransmitter agents; neuromuscular agents; NMJ;
KW   neuromuscular junctions; memory agents; Alzheimers disease;
KW   CNS depressants; CNS stimulators; tranquilisers; muscle relaxants;
KW   antispasmodics; analgesics; anesthetics; anticonvulsants;
KW   antiepileptic agents; antianxiety agents; hallucinogens; sedatives;
KW   hypnotics.
OS   Agrobacterium tumefaciens
PN   US7844304-A.
PD   01-JAN-1993.
PF   28-FEB-1992; 844304.
PR   28-FEB-1992; US-844304.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PI   Kim R,  Wistow G;
DR   WPI; 93-093573/11.
PT   New mu-crystalline proteins - having ornithine cyclo-deaminase
PT   activity, used in diagnosis and treatment of disorders in
PT   ornithine metabolism
PS   Disclosure; Page 34; 60pp; English.
CC   This sequence represents ornithine cyclodeaminase (OCD) from
CC   Agrobacterium Ti plasmid pTiC58. It shows approximately 30%
CC   homology with the kangaroo eye lens protein mu-crystallin.
SQ   Sequence   354 AA;

  Query Match           36.9%;  Score 52;  DB 6;  Length 354;
  Best Local Similarity  63.6%;  Pred. No. 6.06e+01;
  Matches    7;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db    312 ryvrdrvegss 322
          : ||::|||||
Qy     11 KCVRQKVEGSS 21


RESULT   13
ID   R14325 standard; Protein; 589 AA.
AC   R14325;
DT   17-JAN-1992  (first entry)
DE   Rat epithelin precursor.
KW   ET; growth regulation; inhibition; stimulation.
OS   Rattus rattus.
FH   Key             Location/Qualifiers
FT   Protein         1..589
FT   /label= precursor
FT   /note= "claim 11, page 54"
FT   Protein         280..335
FT   /label= EP-1
FT   /note= "claim 12, page 54"
FT   Protein         205..261
FT   /label= EP-2
FT   /note= "claim 13, page 54"
FT   Peptide         59..114
FT   /label= EP
FT   /note= "claim 14, page 54"
FT   Peptide         123..179
FT   /label= EP
FT   /note= "claim 15, page 54"
FT   Peptide         362..416
FT   /label= EP
FT   /note= "claim 16, page 54"
FT   Peptide         440..495
FT   /label= EP
FT   /note= "claim 17, page 54"
FT   Peptide         515..570
FT   /label= EP
FT   /note= "claim 18, page 55"
PN   WO9115510-A.
PD   17-OCT-1991.
PF   03-APR-1991; U02321.
PR   03-APR-1990; US-504508.
PR   13-MAR-1991; US-083796.
PA   (BRIM ) BRISTOL-MYERS SQUIB.
PI   Shoyab M, Plowman GD;
DR   WPI; 91-325168/44.
DR   N-PSDB; Q14338.
PT   New cysteine-rich growth modulating proteins, epithelins - useful
PT   as inhibitors of neoplastic cell growth and to promote wound
PT   healing and treat psoriasis
PS   Disclosure; Fig 18; 97pp; English.
CC   ET-1 is a bifunctional growth regulator, capable of stimulating
CC   the growth of some cell types while inhibiting the growth of others.
CC   ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
CC   bioactivity.  In contrast, however, ET-2 is apparently not capable of
CC   eliciting the growth stimulatory activity characteristic of ET-1 and,
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CC   in fact, antagonises this ET-1 activity.
CC   See also Q14338-40, Q14952-53, R14328-9 and R15315-20.
SQ   Sequence   589 AA;

  Query Match           36.2%;  Score 51;  DB 3;  Length 589;
  Best Local Similarity  46.2%;  Pred. No. 7.71e+01;
  Matches    6;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db    560 hcsakgtkclrkk 572
          | ::|::||:| |
Qy      4 HQGTKSSKCVRQK 16


RESULT   14
ID   R15785 standard; Protein; 914 AA.
AC   R15785;
DT   10-FEB-1992  (first entry)
DE   B.thuringiensis toxin/AcNPV gp64 fusion protein.
KW   chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae;
KW   midgut targetting; bacterial endotoxin; pFAC13.
OS   Bacillus thuringiensis var. tenebriosis.
OS   Autographa californica Nuclear Polyhedrosis Virus.
PN   WO9117254-A.
PD   14-NOV-1991.
PF   02-MAY-1991; U03008.
PR   03-MAY-1990; US-518575.
PA   (REGC ) UNIV OF CALIFORNIA.
PI   Sivasubramanian N, Federici A;
DR   WPI; 91-353775/48.
DR   N-PSDB; Q14808.
PT   Extending host range or toxicity of insecticidal proteins - using
PT   protein capable of binding to gut epithelium of insects
PS   Claim 55; Fig 18; 61pp; English.
CC   A polylinker was inserted into the XmnI restriction site at the
CC   carboxyl terminus coding region of B.thuringiensis var. tenebriosis
CC   (Btt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
CC   was operably linked to the Btt toxin coding sequence via the
CC   polylinker. The gp64 gene sequences act as midgut targetting
CC   signals for bacterial endotoxins. Plasmid pFAC13 was one of three
CC   different Btt/gp64 gene fusions that were constructed and its
CC   deduced amino acid sequence is given here.
CC   See also Q14806 and Q14807.
SQ   Sequence   914 AA;

  Query Match           36.2%;  Score 51;  DB 3;  Length 914;
  Best Local Similarity  45.5%;  Pred. No. 7.71e+01;
  Matches    5;  Conservative    5;  Mismatches   1;  Indels   0;  Gaps   0;

Db    665 kfnrcikrkve 675
          | ::|:::|||
Qy      8 KSSKCVRQKVE 18


RESULT   15
ID   R15784 standard; Protein; 956 AA.
AC   R15784;
DT   10-FEB-1992  (first entry)
DE   B.thuringiensis toxin/AcNPV gp64 fusion protein.
KW   chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae;
KW   midgut targetting; bacterial endotoxin; pFX7.
OS   Bacillus thuringiensis var. tenebriosis.
OS   Autographa californica Nuclear Polyhedrosis Virus.
PN   WO9117254-A.
PD   14-NOV-1991.
PF   02-MAY-1991; U03008.
PR   03-MAY-1990; US-518575.
PA   (REGC ) UNIV OF CALIFORNIA.
PI   Sivasubramanian N, Federici A;
DR   WPI; 91-353775/48.
DR   N-PSDB; Q14807.
PT   Extending host range or toxicity of insecticidal proteins - using
PT   protein capable of binding to gut epithelium of insects
PS   Claim 55; Fig 17; 61pp; English.
CC   A polylinker was inserted into the XmnI restriction site at the
CC   carboxyl terminus coding region of B.thuringiensis var. tenebriosis
CC   (Btt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
CC   was operably linked to the Btt toxin coding sequence via the
CC   polylinker. The gp64 gene sequences act as midgut targetting
CC   signals for bacterial endotoxins. Plasmid pFX7 was one of three
CC   different Btt/gp64 gene fusions that were constructed and its
CC   deduced amino acid sequence is given here.
CC   See also Q14806 and Q14808.
SQ   Sequence   956 AA;

  Query Match           36.2%;  Score 51;  DB 3;  Length 956;
  Best Local Similarity  45.5%;  Pred. No. 7.71e+01;
  Matches    5;  Conservative    5;  Mismatches   1;  Indels   0;  Gaps   0;

Db    707 kfnrcikrkve 717
          | ::|:::|||
Qy      8 KSSKCVRQKVE 18


RESULT   16
ID   R25141 standard; Protein; 986 AA.
AC   R25141;
DT   04-JAN-1993  (first entry)
DE   JAK2.
KW   Phosphorylation; JAK1; JAK2; protein tyrosine kinase; human;
KW   catalytic domain; SH2 domain; growth factor receptor; PTK; murine.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Domain          402..663
FT   /note= "Protein kinase domain 1"
FT   Domain          706..979
FT   /note= "Protein kinase domain 2"
PN   WO9210519-A.
PD   25-JUN-1992.
PF   26-NOV-1991; U08889.
PR   28-NOV-1990; AU-003594.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Harpur A, Wilks AF, Ziemiecki A;
DR   WPI; 92-234591/28.
DR   N-PSDB; Q25307.
PT   Novel protein tyrosine kinase mol. - comprises multiple catalytic
PT   domains but no SH2 domain and is for phosphorylation of proteins
PS   Claim 10; Fig 8; 50pp; English.
CC   This sequence represents the murine protein tyrosine kinase JAK2 (from
CC   Janus kinase).  Northern anlysis of JAK2 expression in a mouse
CC   demonstrated the presence of two mRNA transcripts (4.8 and 4.4 kb).
CC   The levels of these transcripts alter with respect to one another in
CC   different tissues.  Thr kidney, spleen and lung appear to express
CC   predominantly the larger form, whereas ovary, placenta, skeletal muscle
CC   and all murine cell lines analysed express both forms at equal levels.
CC   The difference in sizes may be due to differential polyadenylation
CC   sites.  Both JAK2 and JAK1 are examples of a new subfamily or class
CC   of protein tyrosine kinase.  These can be used in the phosphorylation
CC   of proteins, incorporation of labels and in the design of analogues,
CC   antagonists and agonists of JAK's.
SQ   Sequence   986 AA;

  Query Match           36.2%;  Score 51;  DB 9;  Length 986;
  Best Local Similarity  55.6%;  Pred. No. 7.71e+01;
  Matches    5;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db     68 pkcvrakiq 76
          :|||| |::
Qy     10 SKCVRQKVE 18


RESULT   17
ID   R15783 standard; Protein; 1100 AA.
AC   R15783;
DT   10-FEB-1992  (first entry)
DE   B.thuringiensis toxin/AcNPV gp64 fusion protein.
KW   chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae;
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KW   midgut targetting; bacterial endotoxin; pFAv10.
OS   Bacillus thuringiensis var. tenebriosis.
OS   Autographa californica Nuclear Polyhedrosis Virus.
PN   WO9117254-A.
PD   14-NOV-1991.
PF   02-MAY-1991; U03008.
PR   03-MAY-1990; US-518575.
PA   (REGC ) UNIV OF CALIFORNIA.
PI   Sivasubramanian N, Federici A;
DR   WPI; 91-353775/48.
DR   N-PSDB; Q14806.
PT   Extending host range or toxicity of insecticidal proteins - using
PT   protein capable of binding to gut epithelium of insects
PS   Claim 55; Fig 16; 61pp; English.
CC   A polylinker was inserted into the XmnI restriction site at the
CC   carboxyl terminus coding region of B.thuringiensis var. tenebriosis
CC   (Btt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
CC   was operably linked to the Btt toxin coding sequence via the
CC   polylinker. The gp64 gene sequences act as midgut targetting
CC   signals for bacterial endotoxins. Of three different Btt/gp64 gene
CC   fusions that were constructed, pFAv10 was the longest. Its deduced
CC   amino acid sequence is given here.
CC   See also Q14807 and Q14808.
SQ   Sequence   1100 AA;

  Query Match           36.2%;  Score 51;  DB 3;  Length 1100;
  Best Local Similarity  45.5%;  Pred. No. 7.71e+01;
  Matches     5;  Conservative     5;  Mismatches   1;  Indels   0;  Gaps   0;

Db    851 kfnrcikrkve 861
          | ::|:::|||
Qy      8 KSSKCVRQKVE 18


RESULT   18
ID   R70830 standard; Protein; 1129 AA.
AC   R70830;
DT   06-OCT-1995  (first entry)
DE   Murine JAK2 kinase.
KW   JAK family; protein tyrosine kinase; cytokine receptor; mouse;
KW   phosphorylation; signal transduction; activation.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Region          758..776
FT   /label= epitope
FT   Modified_site   1000-1015
FT   /label= autophosphorylation_site
FT   Misc_difference 1..1129
FT   /note= "Amino acid sequence deduced from the
FT   published partial sequence of Jak2 cDNA
FT   (Harpur et al., Oncogene 7:1347-1353(1992))
FT   differs from R70830 in having the
FT   residues shown in brackets at the following
FT   positions: 154(S), 155(P), 337(T), 341(V),
FT   473(S), 517(V), 522(L), 575(E), 731(T)"
PN   WO9503701-A.
PD   09-FEB-1995.
PF   29-JUL-1994; U08676.
PR   29-JUL-1993; US-097997.
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PI   Ihle JN,  Quelle FW,  Silvennoinen O,  Witthuhn BA;
DR   WPI; 95-081950/11.
DR   N-PSDB; Q85412.
PT   Inhibiting a cellular response to a cytokine by inhibiting Jak
PT   kinase - to treat diseases caused by excessive response to
PT   cytokine, e.g. erythrocytosis and other cellular proliferative
PT   diseases
PS   Claim 1; Fig 1; 167pp; English.
CC   Inhibiting the activity of a jak kinase (pref. Jak1, Jak2, Jak3 or
CC   Tyk2) in a eukaryotic cell is claimed as a method of inhibiting the
CC   biological response of that cell to a cytokine (not IL-3 or
CC   erythropoietin). The present sequence (murine JAK2 kinase) includes
CC   an epitopic sequence at amino acid positions 758-776. Antibodies which
CC   selectively bind the epitope are able to bind Jak2 without interfering
CC   with the activity of the kinase. Such antibodies are claimed and are
CC   useful for detecting and extracting Jak2. There are 9 amino acid
CC   changes noted between the present sequence and the sequence deduced
CC   from the partial cDNA sequence published by Harpur et al., Oncogene 7:
CC   1347-1353 (1992).
SQ   Sequence   1129 AA;

  Query Match           36.2%;  Score 51;  DB 13;  Length 1129;
  Best Local Similarity  55.6%;  Pred. No. 7.71e+01;
  Matches     5;  Conservative     3;  Mismatches   1;  Indels   0;  Gaps   0;

Db    211 pkcvrakiq 219
          :|||| |::
Qy     10 SKCVRQKVE 18


RESULT   19
ID   R88123 standard; Protein; 1144 AA.
AC   R88123;
DT   28-MAR-1996  (first entry)
DE   Tobacco mosaic virus resistance N gene protein.
KW   Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
KW   crop improvement; transgenic plant; crop improvement.
OS   Nicotiana glutinosa.
FH   Key             Location/Qualifiers
FT   Region          1..150
FT   /label= Cytoplasmic_region
FT   Binding_site    216..224
FT   /label= P-loop
FT   /note= "ATP/GTP-binding site motif"
FT   Binding_site    228..229
FT   /label= P-loop
FT   /note= "ATP/GTP binding site motif"
FT   Binding_site    297..302
FT   /label= P-loop
FT   /note= "ATP/GTP binding site motif"
FT   Region          590..928
FT   /label= Leucine-rich_region
FT   /note= "the leucine-rich region (aa 590-928)
FT   includes 13 repeats of approx. 25 aa
FT   length"
PN   WO9535024-A1.
PD   28-DEC-1995.
PF   16-JUN-1995; U07754.
PR   17-JUN-1994; US-261663.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USDA ) US SEC OF AGRIC.
PI   Baker BJ,  Whitham SA;
DR   WPI; 96-058144/06.
DR   N-PSDB; T09341.
PT   Plant virus resistance gene N sequences from tobacco - useful for
PT   generating transgenic Solanaceous plants resistant to Tobacco Mosaic
PT   Virus
PS   Claim 1; Page 65-70; 98pp; English.
CC   The Nicotiana glutinosa N gene protein (R88123) mediates
CC   resistance to tobacco mosaic virus (TMV).  A cDNA clone (T09341)
CC   coding for the protein was obtd. from a N. glutinosa leaf cDNA
CC   library by transposon tagging.  DNA sequences encoding the
CC   protein can be used to generate transgenic plants, esp. Solanaceae,
CC   resistant to TMV.
SQ   Sequence   1144 AA;

  Query Match           36.2%;  Score 51;  DB 15;  Length 1144;
  Best Local Similarity  25.0%;  Pred. No. 7.71e+01;
  Matches     4;  Conservative     6;  Mismatches   6;  Indels   0;  Gaps   0;

Db    156 dnrdktdadcirqiid 171
          |::    : |:|| ::
Qy      3 DHQGTKSSKCVRQKVE 18


RESULT   20
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ID   R88122 standard; Protein; 1144 AA.
AC   R88122;
DT   28-MAR-1996  (first entry)
DE   Tobacco mosaic virus resistance N gene protein.
KW   Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
KW   crop improvement; transgenic plant; crop improvement.
OS   Nicotiana glutinosa.
FH   Key             Location/Qualifiers
FT   Region          1..150
FT   /label= Cytoplasmic_region
FT   Binding_site    216..224
FT   /label= P-loop
FT   /note= "ATP/GTP-binding site motif"
FT   Binding_site    228..229
FT   /label= P-loop
FT   /note= "ATP/GTP binding site motif"
FT   Binding_site    297..302
FT   /label= P-loop
FT   /note= "ATP/GTP binding site motif"
FT   Region          590..928
FT   /label= Leucine-rich_region
FT   /note= "the leucine-rich region (aa 590-928)
FT   includes 13 repeats of approx. 25 aa
FT   length"
PN   WO9535024-A1.
PD   28-DEC-1995.
PF   16-JUN-1995; U07754.
PR   17-JUN-1994; US-261663.
PA   (REGC ) UNIV CALIFORNIA.
PA   (USDA ) US SEC OF AGRIC.
PI   Baker BJ,  Whitham SA;
DR   WPI; 96-058144/06.
DR   N-PSDB; T09340.
PT   Plant virus resistance gene N sequences from tobacco - useful for
PT   generating transgenic Solanaceous plants resistant to Tobacco Mosaic
PT   Virus
PS   Example 6; Page 52-60; 98pp; English.
CC   The Nicotiana glutinosa N gene protein (R88123) mediates
CC   resistance to tobacco mosaic virus (TMV).  The gene (T09341)
CC   coding for the protein was obtd. from a N. glutinosa leaf genomic
CC   library by screening with a cDNA clone.  DNA sequences encoding the
CC   protein can be used to generate transgenic plants, esp. Solanaceae,
CC   resistant to TMV.
SQ   Sequence   1144 AA;

  Query Match           36.2%;  Score 51;  DB 15;  Length 1144;
  Best Local Similarity  25.0%;  Pred. No. 7.71e+01;
  Matches    4;  Conservative    6;  Mismatches   6;  Indels   0;  Gaps   0;

Db    156 dnrdktdadcirqiid 171
          |::    : |:|| ::
Qy      3 DHQGTKSSKCVRQKVE 18


RESULT   21
ID   R46605 standard; Protein; 1588 AA.
AC   R46605;
DT   22-SEP-1994  (first entry)
DE   Malarial PfEMP3 epitopic fragment.
KW   Plasmodium falciparum erythrocyte membrane protein; PfEMP3;
KW   malaria; antigen; epitope; vaccine; anti-idiotype antibody.
OS   Plasmodium falciparum (Malayan Camp strain).
PN   WO9403604-A.
PD   17-FEB-1994.
PF   05-AUG-1993; U07261.
PR   07-AUG-1992; US-927531.
PA   (SCHE ) SCHERING CORP.
PI   Handunnetti SM,  Howard RJ,  Pasloske BL,  Van Schravendijk MR;
DR   WPI; 94-065693/08.
DR   N-PSDB; Q70102.
PT   New malaria antigen, PfEMP3 - used to isolate and produce prods.
PT   for use in diagnosis, therapy and prevention of malarial
PT   infection
PS   Claim 12; Page 79-85; 79pp; English.
CC   The PfEMP3 malarial antigen is recognised by monoclonal antibody MAb
CC   12C11. Nucleic acid sequences encoding part of the 315kD antigen,
CC   have been isolated and sequenced. PfEMP3 is encoded on chromosome 2
CC   of the P.falciparum genome and is thought to be associated with knob
CC   formation and structure; malarial strains carrying deletions of the
CC   gene coding for PfEMP3 exhibit a knobless phenotype.
SQ   Sequence   1588 AA;

  Query Match           36.2%;  Score 51;  DB 9;  Length 1588;
  Best Local Similarity  31.6%;  Pred. No. 7.71e+01;
  Matches    6;  Conservative    7;  Mismatches   6;  Indels   0;  Gaps   0;

Db     44 esqdsssekslkekvngea 62
          : | : | | :::||:| :
Qy      3 DHQGTKSSKCVRQKVEGSS 21


RESULT   22
ID   R46608 standard; Protein; 1663 AA.
AC   R46608;
DT   22-SEP-1994  (first entry)
DE   Plasmodium falciparum erythrocyte membrane protein PfEMP3.
KW   Plasmodium falciparum erythrocyte membrane protein; PfEMP3;
KW   malaria; antigen; epitope; vaccine; anti-idiotype antibody.
OS   Plasmodium falciparum (Malayan Camp strain).
FH   Key             Location/Qualifiers
FT   Region          472..493
FT   /label= tandem_repeat
FT   /note= "one of 21 complete segments of homology
FT   of 22 amino acid length"
FT   Region          494..515
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FT   of 22 amino acid length"
FT   Region          516..537
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FT   Region          538..559
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FT   of 22 amino acid length"
FT   Region          560..581
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FT   of 22 amino acid length"
FT   Region          648..669
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FT   Region          670..691
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FT   Region          692..713
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FT   Region          714..735
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  Best Local Similarity  31.6%;  Pred. No. 7.71e+01;
  Matches    6;  Conservative    7;  Mismatches   6;  Indels   0;  Gaps   0;

Db     44 esqdssseksslkekvngea 62
          : | : | | :::||:| :
Qy      3 DHQGTKSSKCVRQKVEGSS 21


RESULT   23
ID   R50036 standard; Protein; 429 AA.
AC   R50036;
DT   17-OCT-1994  (first entry)
DE   Hantaian virus Nucleocapsid N protein.
KW   Nucleocapsid N protein; G1; G2; glycoprotein; vector; vaccine;
KW   diagnosis; korean hemorrhagic fever; antibody.
OS   Hantaan virus.
FH   Key             Location/Qualifiers
FT   Misc_difference 122..123
FT   /note= "Encoded by ACT ACT"
FT   Misc_difference 195
FT   /note= "Encoded by CTT"
FT   Misc_difference 224
FT   /note= "Encoded by GTT"
FT   Misc_difference 233
FT   /note= "Encoded by ATG"
FT   Misc_difference 422
FT   /note= "Encoded by TTC"
PN   US5298423-A.
PD   29-MAR-1994.
PF   25-NOV-1987; 125105.
PR   25-NOV-1987; US-125105.
PR   14-NOV-1991; US-799479.
PA   (USSA ) US SEC OF ARMY.
PI   Dalrymple JM,  Schmaljohn CS;
DR   WPI; 94-100339/12.
DR   N-PSDB; Q58735.
PT   Vectors contg. coding sequences for the Hantaan virus
PT   nucleo-capsid N protein or G1 and G2 glyco-protein precursor -
PT   generate viral proteins without having to propagate live
PT   infectious virus
PS   Disclosure; Fig 2; 23pp; English.
CC   This sequence represents the Hantaian virus nucleocapsid N protein.
CC   The cDNA encoding this sequence may be introduced into a vector for
CC   the production of Hantaan virus proteins without the need to propagate
CC   live virus.  The expressed protein can be used in vaccines and
CC   diagnostic applications for the study of korean hemorrhagic fever.
CC   The protein can also be injected into animals to raise antibodies
CC   against the virus.
SQ   Sequence   429 AA;

  Query Match           34.8%;  Score 49;  DB 10;  Length 429;
  Best Local Similarity  35.0%;  Pred. No. 1.24e+02;
  Matches    7;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db    273 lgnmetkeskairqhaeaag 292
          : :  || || :||  |:::
Qy      2 IDHQGTKSSKCVRQKVEGSS 21


RESULT   24
ID   R13794 standard; Protein; 487 AA.
AC   R13794;
DT   29-NOV-1991  (first entry)
DE   Drosophila hormone receptor 3.
KW   Insect steroid receptor; DHR3.
OS   Drosophila melanogaster.
FH   Key             Location/Qualifiers
FT   Domain          51..116
FT   /note= "zinc-finger DNA-binding domain C"
FT   Domain          255..479
FT   /note= "hormone-binding domain E"
PN   WO9113167-A.
PD   05-SEP-1991.
PF   15-FEB-1991; U01189.
PR   26-FEB-1990; US-485749.
PA   (STRD ) LELAND STANFORD JR UNIV.
PI   Hogness DS, Koelle MR, Segraves WA;
DR   WPI; 91-281480/38.
DR   N-PSDB; Q13575.
PT   DNA encoding insect steroid receptors - and ligands, for use as
PT   benign inducing factors
PS   Claim 24; Page 103; 126pp; English.
CC   The amino acid sequence codes for Drosophila hormone receptor 3
CC   protein which is part of the insect steroid receptor superfamily.
CC   It can be used to screen for ligands specific for the insect
CC   steroid receptors which can be used as highly specific and highly
CC   active pesticides which are biodegradable. See also R13791-R13793.
SQ   Sequence   487 AA;

  Query Match           34.8%;  Score 49;  DB 3;  Length 487;
  Best Local Similarity  27.8%;  Pred. No. 1.24e+02;
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Db     82 vvnyqcprnkqcvvdrvn 99
          |:: |  ::  || ::|:
Qy      1 VIDHQGTKSSKCVRQKVE 18


RESULT   25
ID   R04107 standard; protein; 694 AA.
AC   R04107;
DT   13-SEP-1990  (first entry)
DE   DNA-binding protein GCF represses transcription when bound to GC-rich seq
KW   DNA-binding protein; GC-rich promoters; repression of transcription; ss
OS   synthetic.
FH   Key             Location/Qualifiers
FT   binding_site    359
FT   /label= putative leucine zipper
FT   binding_site    366
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PN   US7441912-A.
PD   06-MAR-1990.
PF   28-NOV-1989; 134693.
PR   28-NOV-1989; US-441912.
PA   (USSH) US National Cancer Institute.
PI   Pastan I, Kageyama R;
DR   WPI; 90-132048/17.
DR   N-NSDB; Q04026.
PT   DNA binding protein recognises GC-rich sequences and represses
PT   transcription from GC-rich promoters when bound to them
PS   Disclosure; p; English.
CC   The protein recognises GC-rich promoters including those of housekeeping
```

CC genes and cellular oncogenes.
SQ Sequence 694 AA;

Query Match 34.8%; Score 49; DB 1; Length 694;
Best Local Similarity 52.9%; Pred. No. 1.24e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy      5 QGTKSSKCVRQKVEGSS 21
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FILE 'REGISTRY' ENTERED AT 10:20:16 ON 29 JUL 1997
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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DICTIONARY FILE UPDATES: 28 JULY 97  HIGHEST RN 191786-00-2

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  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

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L1   ANSWER 1 OF 6  REGISTRY  COPYRIGHT 1997 ACS
RN   173012-07-2  REGISTRY
CN   Complement C5, prepro- (human) (9CI)  (CA INDEX NAME)
FS   PROTEIN SEQUENCE
SQL  1676

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       151 DLKPAKRETV LTFIDPEGSE VDMVEEIDHI GIISFPDFKI PSNPRYGMWT
       201 IKAKYKEDFS TTGTAYFEVK EYVLPHFSVS IEPEYNFIGY KNFKNFEITI
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       351 PYKLNLVATP LFLKPGIPYP IKVQVKDSLD QLVGGVPVIL NAQTIDVNQE
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       501 YLILSKGKII HFGTREKFSD ASYQSINIPV TQNMVPSSRL LVYYIVTGEQ
       551 TAELVSDSVW LNIEEKCGNQ LQVHLSPDAD AYSPGQTVSL NMATGMDSWV
       601 ALAAVDSAVY GVQRGAKKPL ERVFQFLEKS DLGCGAGGGL NNANVFHLAG
       651 LTFLTNANAD DSQENDEPCK EILRPRRTLQ KKIEEIAAKY KHSVVKKCCY
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       751 RLHMKTLLPV SKPEIRSYFP ESWLWEVHLV PRRKQLQFAL PDSLTTWEIQ
       801 GIGISNTGIC VADTVKAKVF KDVFLEMNIP YSVVRGEQIQ LKGTVYNYRT
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      1151 GIRKAFDICP LVKIDTALIK ADNFLLENTL PAQSTFTLAI SAYALSLGDK
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      1251 TAYALLTSLN LKDINYVNPV IKWLSEEQRY GGGFYSTQDT INAIEGLTEY
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      1351 GFGSGLATVH VTTVVHKTST SEEVCSFYLK IDTQDIEASH YRGYGNSDYK
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1651 DTTCSSCQAF LANLDEFAED IFLNGC
HITS AT: 872-892
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 2 OF 6 REGISTRY COPYRIGHT 1997 ACS
RN 172998-82-2 REGISTRY
CN L-Serine, L-valyl-L-isoleucyl-L-.alpha.-aspartyl-L-histidyl-L-glutaminylglycyl-L-threonyl-L-lysyl-L-seryl-L-seryl-L-lysyl-L-cysteinyl-L-valyl-L-arginyl-L-glutaminyl-L-lysyl-L-valyl-L-.alpha.-glutamylglycyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 21

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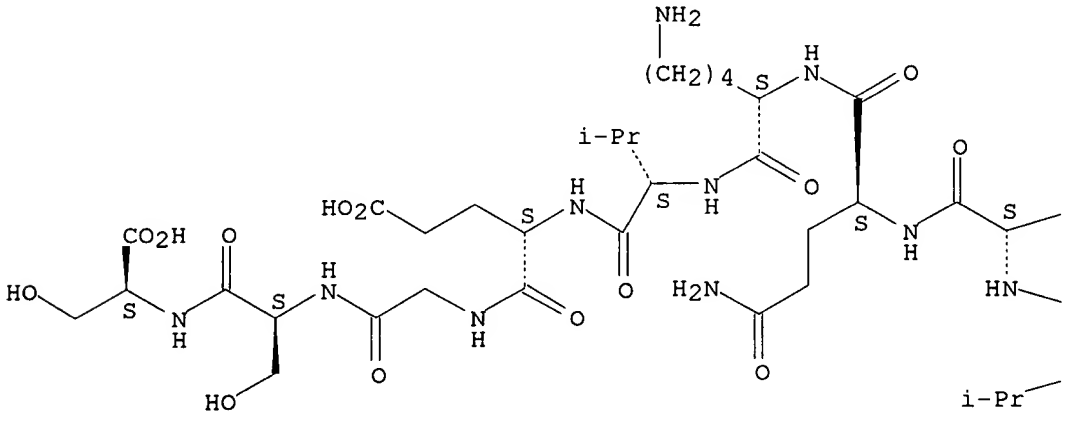
SR CA
LC STN Files: CA, CAPLUS, TOXLIT

Absolute stereochemistry.

PAGE 1-A



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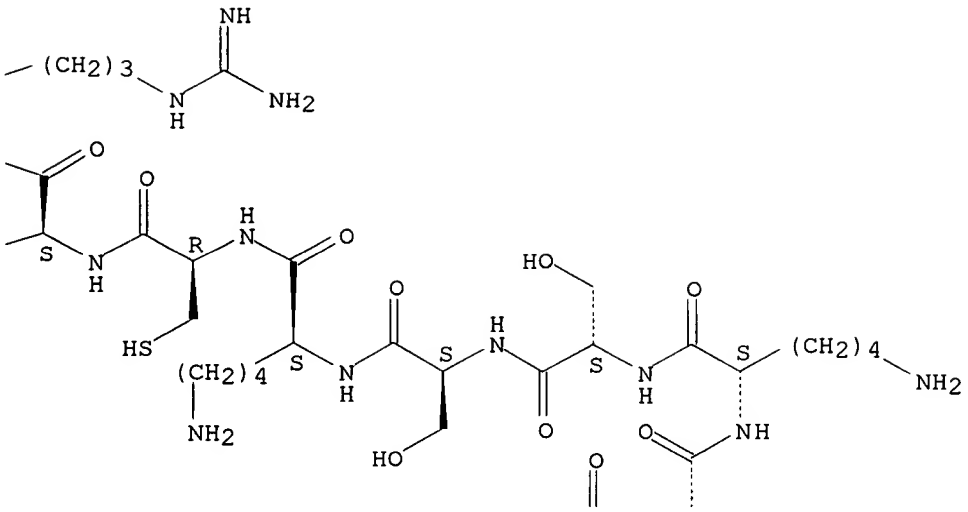

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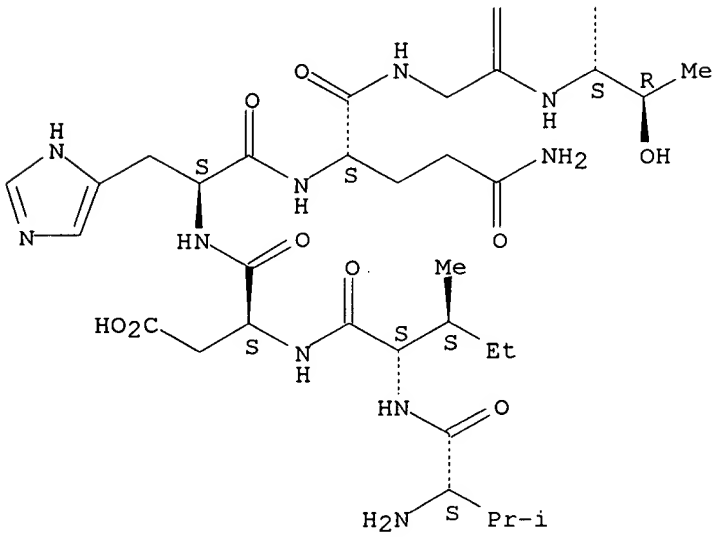

1 REFERENCES IN FILE CA (1967 TO DATE)
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L1 ANSWER 3 OF 6 REGISTRY COPYRIGHT 1997 ACS
RN 134774-08-6 REGISTRY
CN Complement C5, pro- (human clone pHC5A/pC5HG2 protein moiety reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE
SQL 1658

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    151 SEVDMVEEID HIGIISFPDF KIPSNPRYGM WTIKAKYKED FSTTGTAYFE
    201 VKEYVLPHFS VSIEPEYNFI GYKNFKNFEI TIKARYFYNK VVTEADVYIT
    251 FGIREDLKDD QKEMMQTAMQ NTMLINGIAQ VTFDSETAVK ELSYYSLEDL
    301 NNKYLYIAVT VIESTGGFSE EAEIPGIKYV LSPYKLNLVA TPLFLKPGIP
    351 YPIKVQVKDS LDQLVGGVPV ILNAQTIDVN QETSDLDPSK SVTRVDDGVA
    401 SFVLNLPSGV TVLEFNVKTD APDLPEENQA REGYRAIAYS SLSQSYLYID
    451 WTDNHKALLV GEHLNIIVTP KSPYIDKITH YNYLILSKGK IIHFGTREKF
    501 SDASYQSINI PVTQNMVPSS RLLVYYIVTG EQTAELVSDS VWLNIEEKCG
    551 NQLQVHLSPD ADAYSPGQTV SLNMATGMDS WVALAAVDSA VYGVQRGAKK
    601 PLERVFQFLE KSDLGCGAGG GLNNANVFHL AGLTFLTNAN ADDSQENDEP
    651 CKEILRPRRT LQKKIEEIAA KYKHSVVKKC CYDGACVNND ETCEQRAARI
    701 SLGPRCIKAF TECCVVASQL RANISHKDMQ LGRLHMKTLL PVSKPEIRSY
    751 FPESWLWEVH LVPRRKQLQF ALPDSLTTWE IQGIGISNTG ICVADTVKAK
    801 VFKDVFLEMN IPYSVVRGEQ IQLKGTVYNY RTSGMQFCVK MSAVEGICTS
    851 ESPVIDHQGT KSSKCVRQKV EGSSSHLVTF TVLPLEIGLH NINFSLETWF
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    901 GKEILVKTLR VVPEGVKRES YSGVTLDPRG IYGTISRRKE FPYRIPLDLV
    951 PKTEIKRILS VKGLLVGFIL SAVLSQEGIN ILTHLPKGSA EAELMSVVPV
   1001 FYVFHYLETG NHWNIFHSDP LIEKQKLKKK LKEGMLSIMS VRNADYSYSV
   1051 WKGGSASTWL TAFALRVLGQ VNKYVEQNQN SICNSLLWLV ENYQLDNGSF
   1101 KENSQYQPIK LQGTLPVEAR ENSLYLTAFT VIGIRKAFDI CPLVKIDTAL
   1151 IKADNFLLEN TLPAQSTFTL AISAYALSLG DKTHPQFRSI VSALKREALV
   1201 KGNPPIYRFW KDNLQHKDSS VPNTGTARMV ETTAYALLTS LNLKDINYVN
   1251 PVIKWLSEEQ RYGGGFYSTQ DTINAIEGLT EYSLLVKQLR LSMDIDVSYK
   1301 HKGALHNYKM TDKNFLGRPV EVLLNDDLIV STGFGSGLAT VHVTTVVHKT
   1351 STSEEVCSFY LKIDTQDIEA SHYRGYGNSD YKRIVACASY KPSREESSSG
   1401 SSHAVMDISL PTGISANEED LKALVEGVDQ LFTDYQIKDG HVILQLNSIP
   1451 SSDFLCVRFR IFELFEVGFL SPATFTVYEY HRPDKQCTMF YSTSNIKIQK
   1501 VCEGAACKCV EADCGQMQEE LDLTISAETR KQTACKPEIA YAYKVSITSI
   1551 TVENVFVKYK ATLLDIYKTG EAVAFKDSEI TFIKKVTCTN AELVKGRQYL
   1601 IMGKEALQIK YNFSFRYIYP LDSLTWIEYW PRDTTCSSCQ AFLANLDEFA
   1651 EDIFLNGC
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HITS AT: 854-874
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1 ANSWER 4 OF 6 REGISTRY COPYRIGHT 1997 ACS
RN 134774-06-4 REGISTRY
CN Complement C5, prepro- (human clone pHC5A/pC5HG2 protein moiety reduced) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 1676

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      1 MGLLGILCFL IFLGKTWGQE QTYVISAPKI FRVGASENIV IQVYGYTEAF
     51 DATISIKSYP DKKFSYSSGH VHLSSEVKFQ NSAILTIQPK QLPGGQNPVS
    101 YVYLEVVSKH FSKSKRMPIT YDNGFLFIHT DKPVYTPDQS VKVRVYSLND
    151 DLKPAKRETV LTFIDPEGSE VDMVEEIDHI GIISFPDFKI PSNPRYGMWT
    201 IKAKYKEDFS TTGTAYFEVK EYVLPHFSVS IEPEYNFIGY KNFKNFEITI
    251 KARYFYNKVV TEADVYITFG IREDLKDDQK EMMQTAMQNT MLINGIAQVT
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       301 FDSETAVKEL SYYSLEDLNN KYLYIAVTVI ESTGGFSEEA EIPGIKYVLS
       351 PYKLNLVATP LFLKPGIPYP IKVQVKDSLD QLVGGVPVIL NAQTIDVNQE
       401 TSDLDPSKSV TRVDDGVASF VLNLPSGVTV LEFNVKTDAP DLPEENQARE
       451 GYRAIAYSSL SQSYLYIDWT DNHKALLVGE HLNIIVTPKS PYIDKITHYN
       501 YLILSKGKII HFGTREKFSD ASYQSINIPV TQNMVPSSRL LVYYIVTGEQ
       551 TAELVSDSVW LNIEEKCGNQ LQVHLSPDAD AYSPGQTVSL NMATGMDSWV
       601 ALAAVDSAVY GVQRGAKKPL ERVFQFLEKS DLGCGAGGGL NNANVFHLAG
       651 LTFLTNANAD DSQENDEPCK EILRPRRTLQ KKIEEIAAKY KHSVVKKCCY
       701 DGACVNNDET CEQRAARISL GPRCIKAFTE CCVVASQLRA NISHKDMQLG
       751 RLHMKTLLPV SKPEIRSYFP ESWLWEVHLV PRRKQLQFAL PDSLTTWEIQ
       801 GIGISNTGIC VADTVKAKVF KDVFLEMNIP YSVVRGEQIQ LKGTVYNYRT
       851 SGMQFCVKMS AVEGICTSES PVIDHQGTKS SKCVRQKVEG SSSHLVTFTV
                                ========= ========== ==
       901 LPLEIGLHNI NFSLETWFGK EILVKTLRVV PEGVKRESYS GVTLDPRGIY
       951 GTISRRKEFP YRIPLDLVPK TEIKRILSVK GLLVGFILSA VLSQEGINIL
      1001 THLPKGSAEA ELMSVVPVFY VFHYLETGNH WNIFHSDPLI EKQKLKKKLK
      1051 EGMLSIMSVR NADYSYSVWK GGSASTWLTA FALRVLGQVN KYVEQNQNSI
      1101 CNSLLWLVEN YQLDNGSFKE NSQYQPIKLQ GTLPVEAREN SLYLTAFTVI
      1151 GIRKAFDICP LVKIDTALIK ADNFLLENTL PAQSTFTLAI SAYALSLGDK
      1201 THPQFRSIVS ALKREALVKG NPPIYRFWKD NLQHKDSSVP NTGTARMVET
      1251 TAYALLTSLN LKDINYVNPV IKWLSEEQRY GGGFYSTQDT INAIEGLTEY
      1301 SLLVKQLRLS MDIDVSYKHK GALHNYKMTD KNFLGRPVEV LLNDDLIVST
      1351 GFGSGLATVH VTTVVHKTST SEEVCSFYLK IDTQDIEASH YRGYGNSDYK
      1401 RIVACASYKP SREESSSGSS HAVMDISLPT GISANEEDLK ALVEGVDQLF
      1451 TDYQIKDGHV ILQLNSIPSS DFLCVRFRIF ELFEVGFLSP ATFTVYEYHR
      1501 PDKQCTMFYS TSNIKIQKVC EGAACKCVEA DCGQMQEELD LTISAETRKQ
      1551 TACKPEIAYA YKVSITSITV ENVFVKYKAT LLDIYKTGEA VAFKDSEITF
      1601 IKKVTCTNAE LVKGRQYLIM GKEALQIKYN FSFRYIYPLD SLTWIEYWPR
      1651 DTTCSSCQAF LANLDEFAED IFLNGC
HITS AT:   872-892
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS, TOXLIT
                1 REFERENCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1   ANSWER 5 OF 6  REGISTRY  COPYRIGHT 1997 ACS
RN   112548-72-8  REGISTRY
CN   Complement C5b (human clone pC5HG2 .alpha.'-chain protein moiety
     reduced) (9CI)  (CA INDEX NAME)
FS   PROTEIN SEQUENCE
SQL  925

SEQ      1 LHMKTLLPVS KPEIRSYFPE SWLWEVHLVP RRKQLQFALP DSLTTWEIQG
        51 IGISNTGICV ADTVKAKVFK DVFLEMNIPY SVVRGEQIQL KGTVYNYRTS
       101 GMQFCVKMSA VEGICTSESP VIDHQGTKSS KCVRQKVEGS SSHLVTFTVL
                                ========== ========== =
       151 PLEIGLHNIN FSLETWFGKE ILVKTLRVVP EGVKRESYSG VTLDPRGIYG
       201 TISRRKEFPY RIPLDLVPKT EIKRILSVKG LLVGEILSAV LSQEGINILT
       251 HLPKGSAEAE LMSVVPVFYV FHYLETGNHW NIFHSDPLIE KQKLKKKLKE
       301 GMLSIMSYRN ADYSYSVWKG GSASTWLTAF ALRVLGQVNK YVEQNQNSIC
       351 NSLLWLVENY QLDNGSFKEN SQYQPIKLQG TLPVEARENS LYLTAFTVIG
       401 IRKAFDICPL VKIDTALIKA DNFLLENTLP AQSTFTLAIS AYALSLGDKT
       451 HPQFRSIVSA LKREALVKGN PPIYRFWKDN LQHKDSSVPN TGTARMVETT
       501 AYALLTSLNL KDINYVNPVI KWLSEEQRYG GGFYSTQDTI NAIEGLTEYS
       551 LLVKQLRLSM DIDVSYKHKG ALHNYKMTDK NFLGRPVEVL LNDDLIVSTG
       601 FGSGLATVHV TTVVHKTSTS EEVCSFYLKI DTQDIEASHY RGYGNSDYKR
       651 IVACASYKPS REESSSGSSH AVMDISLPTG ISANEEDLKA LVEGVDQLFT
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       701 DYQIKDGHVI LQLNSIPSSD FLCVRFRIFE LFEVGFLSPA TFTVYEYHRP
       751 DKQCTMFYST SNIKIQKVCE GAACKCVEAD CGDMQEELDL TISAETRKQT
       801 ACKPEIAYAY KVSITSITVE NVFVKYKATL LDIYKTGEAV AEKDSEITFI
       851 KKVTCTNAEL VKGRQYLIMG KEALQIKYNF SFRYIYPLDS LTWIEYWPRD
       901 TTCSSCQAFL ANLDEFAEDI FLNGC
HITS AT:   121-141
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS, CJACS, TOXLIT
                1 REFERENCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L1   ANSWER 6 OF 6  REGISTRY  COPYRIGHT 1997 ACS
RN   112548-71-7  REGISTRY
CN   Complement C5 (human clone pC5HG2 .alpha.-chain protein moiety
     reduced) (9CI)  (CA INDEX NAME)
FS   PROTEIN SEQUENCE
SQL  999

SEQ      1 TLQKKIEEIA AKYKHSVVKK CCYDGACVNN DETCEQRAAR ISLGPRCIKA
        51 FTECCVVASQ LRANISHKDM QLGRLHMKTL LPVSKPEIRS YFPESWLWEV
       101 HLVPRRKQLQ FALPDSLTTW EIQGIGISNT GICVADTVKA KVFKDVFLEM
       151 NIPYSVVRGE QIQLKGTVYN YRTSGMQFCV KMSAVEGICT SESPVIDHQG
                                                       ======
       201 TKSSKCVRQK VEGSSSHLVT FTVLPLEIGL HNINFSLETW FGKEILVKTL
           ========== =====
       251 RVVPEGVKRE SYSGVTLDPR GIYGTISRRK EFPYRIPLDL VPKTEIKRIL
       301 SVKGLLVGEI LSAVLSQEGI NILTHLPKGS AEAELMSVVP VFYVFHYLET
       351 GNHWNIFHSD PLIEKQKLKK KLKEGMLSIM SYRNADYSYS VWKGGSASTW
       401 LTAFALRVLG QVNKYVEQNQ NSICNSLLWL VENYQLDNGS FKENSQYQPI
       451 KLQGTLPVEA RENSLYLTAF TVIGIRKAFD ICPLVKIDTA LIKADNFLLE
       501 NTLPAQSTFT LAISAYALSL GDKTHPQFRS IVSALKREAL VKGNPPIYRF
       551 WKDNLQHKDS SVPNTGTARM VETTAYALLT SLNLKDINYV NPVIKWLSEE
       601 QRYGGGFYST QDTINAIEGL TEYSLLVKQL RLSMDIDVSY KHKGALHNYK
       651 MTDKNFLGRP VEVLLNDDLI VSTGFGSGLA TVHVTTVVHK TSTSEEVCSF
       701 YLKIDTQDIE ASHYRGYGNS DYKRIVACAS YKPSREESSG GGGHAVMDIS
       751 LPTGISANEE DLKALVEGVD QLFTDYQIKD GHVILQLNSI PSSDFLCVRF
       801 RIFELFEVGF LSPATFTVYE YHRPDKQCTM FYSTSNIKIQ KVCEGAACKC
       851 VEADCGQMQE ELDLTISAET RKQTACKPEI AYAYKVSITG ITVENVFVKY
       901 KATLLDIYKT GEAVAEKDSE ITFIKKVTCT NAELVKGRQY LIMGKEALQI
       951 KYNFSFRYIY PLDSLTWIEY WPRDTTCSSC QAFLANLDEF AEDIFLNGC
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CI   MAN
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FILE LAST UPDATED: 29 Jul 1997 (970729/ED)

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L2 3 L1

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L2 ANSWER 1 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:73261 HCAPLUS
DN 124:127101
TI Anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases
IN Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven H.; Rollins, Scott; Rother, Russell P.; Springhorn, Jeremy P.; Squinto, Stephen P.; Thomas, Thomas C.; et al.
PA Alexion Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 159 pp.
CODEN: PIXXD2
PI WO 9529697 A1 951109
DS W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UG, US, UZ, VN
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
AI WO 95-US5688 950501
PRAI US 94-236208 940502
DT Patent
LA English
AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathol. conditions assocd. with GN. Also disclosed are novel anti-C5 antibodies and anti-C5 antibody-encoding nucleic acid mols. These antibodies are useful in the treatment of GN and other inflammatory conditions involving pathol. activation of the complement system.
IT **173012-07-2**, Complement C5, prepro- (human)
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT **172998-82-2P**
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IC ICM A61K038-36
ICS A61K039-00; A61K039-395; C07K014-00; C07K014-75; C07K016-00; C07K016-18; C07K016-36; C07K016-46; C12N005-10; C12N005-20; C12N015-09; C12N015-10; C12N015-13; C12N015-63; C12P021-02;

C12P021-08
CC 63-3 (Pharmaceuticals)
Section cross-reference(s): 3, 15
IT **173012-07-2**, Complement C5, prepro- (human)
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT **172998-82-2P**
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

L2 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1991:442982 HCAPLUS
DN 115:42982
TI Complete cDNA sequence of human complement pro-C5. Evidence of truncated transcripts derived from a single copy gene
AU Haviland, David L.; Haviland, Joie C.; Fleischer, Daniel T.; Hunt, Allison; Wetsel, Rick A.
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO J. Immunol. (1991), 146(1), 362-8
CODEN: JOIMA3; ISSN: 0022-1767
DT Journal
LA English
AB Two truncated human C5 clones, pHC5A and pHC5B, were isolated from an adult human liver cDNA library, and contained inserts of 2930 and 2181 bp, resp. Both clones were polyadenylated and encoded the 5'-end of the C5 pro-mol., thereby completing the human pro-C5 cDNA sequence. However, near the 3'-ends, at exon/intron boundaries, the nucleotide sequences of pHC5A and pHC5B diverged from each other and from the full-length 6.0-kb C5 cDNA sequence. Clone pHC5A, which overlapped the first human C5 clone described (J-16), encoded most of the C5 signal peptide, the complete .beta.-chain, the linker peptide, 177 amino acids of the .alpha.-chain, and contained 144 bp of Alu family consensus sequence encoding 48 amino acids of divergent protein sequence in an open reading frame. Clone pHC5B encoded the entire C5 signal peptide, the .beta.-chain, the linker peptide, 9 amino acids of the .alpha.-chain, and 6 amino acids of divergent protein sequence in an open reading frame. Northern blot expts. demonstrated the presence of a 3.0-kb truncated C5 mRNA in adult human liver and a 4.8-kb truncated C5 mRNA in HepG2 cells in addn. to the 6.0-kb full-length transcript. Truncated C5 mRNA were not detected in Raji, MOLT-4, human fibroblast or U937 cells, although the full-length 6.0-kb transcript was seen in MOLT-4 cells. Southern blot analyses indicated that the human C5 structural gene is large, complex, and is present in the human genome in a single copy, thereby demonstrating that the truncated C5 clones and mRNA are derived from a single C5 gene by alternative processing events.
IT **112548-71-7**, Complement C 5 (human clone pC5HG2 .alpha.-chain protein moiety reduced) **134774-06-4** **134774-08-6**
RL: PRP (Properties)
(amino acid sequence of)
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 13, 15

IT **112548-71-7**, Complement C 5 (human clone pC5HG2 .alpha.-chain protein moiety reduced) 134774-03-1, Complement C 5 (human clone pHC5A/pC5HG2 .beta.-chain protein moiety reduced) 134774-04-2, Complement C 5 (human clone pHC5B protein moiety reduced) 134774-05-3 **134774-06-4** 134774-07-5 **134774-08-6** 134774-09-7 134774-10-0
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1988:107290 HCAPLUS
DN 108:107290
TI Molecular analysis of human complement component C5: localization of the structural gene to chromosome 9
AU Wetsel, Rick A.; Lemons, Richard S.; Le Beau, Michelle M.; Barnum, Scott R.; Noack, Deborah; Tack, Brian F.
CS Dep. Immunol., Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA
SO Biochemistry (1988), 27(5), 1474-82
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
OS CJACS
AB A human C5 clone (pC5HG2) was isolated from a cDNA library constructed from HepG2 mRNA. The DNA sequence showed that the pC5HG2 insert was comprised of 3309 base pairs of pro-C5 coding sequence and 404 base pairs of 3'-untranslated sequence. The derived amino acid sequence contained the entire coding sequence of the C5 .alpha.-chain, the .beta.-.alpha.-chain junction region, and 100 amino acids (.apprx.50%) of the .beta.-chain. Protein sequences of 4 C5 tryptic peptides were aligned exactly to this sequence and demonstrated that C5 synthesized and secreted by HepG2 cells is probably identical with plasma-derived C5. Coding sequence alignment of the human C5 sequences with those of murine C5 indicated that 80% of the nucleotides and 79% of the amino acids were placed identically in the 2 species. Amino acid sequence alignment of the homologous family members C3, C4, and .alpha.2-macroglobulin with that of C5 demonstrated 27%, 25%, and 19% identity, resp. As was found in murine C5, the corresponding thiol ester region of human C5 contained several conserved amino acids, but the crit. cysteine and glutamine residues which give rise to the intramol. thiol ester bond in C3, C4, and .alpha.2-macroglobulin were absent in C5, having been replaced by serine and alanine, resp. With the use of a panel of hamster-human somatic cell hybrids, the C5 gene was mapped to human chromosome 9. In situ chromosomal hybridization studies employing metaphase cells further localized the gene to bands 9q32-34, with the largest cluster of grains at 9q34.1.
IT **112548-71-7 112548-72-8**
RL: PRP (Properties)
(amino acid sequence of)
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 13, 15
IT **112548-71-7 112548-72-8**
RL: PRP (Properties)
(amino acid sequence of)

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FILE LAST UPDATED: 23 JUL 97                <970723/UP>
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DERWENT WEEK FOR CHEMICAL CODING:    9724
DERWENT WEEK FOR POLYMER INDEXING:   9727
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L1            66 SEA FILE=WPIDS ABB=ON  "EVANS M"/AU OR ("EVANS M J"/AU OR
                 "EVANS M J W"/AU)
L2             5 SEA FILE=WPIDS ABB=ON  ("MATIS L"/AU OR "MATIS L A"/AU)
L3           303 SEA FILE=WPIDS ABB=ON  "MUELLER E"/AU OR "MUELLER E E"/AU

L4             5 SEA FILE=WPIDS ABB=ON  "NYE S"/AU OR "NYE S H"/AU
L5            12 SEA FILE=WPIDS ABB=ON  ("ROLLINS S"/AU OR "ROLLINS S A"/A
                 U OR "ROLLINS S M"/AU OR "ROLLINS S S"/AU)
L6           381 SEA FILE=WPIDS ABB=ON  L1 OR L2 OR L3 OR L4 OR L5



     (FILE 'WPIDS' ENTERED AT 09:49:50 ON 29 JUL 1997)
L7            24 S COMPLEMENT AND C5
L8             3 S L7 AND L6
L9           309 S ALPHA (2W) CHAIN#
L10            1 S L7 AND L9
L11        14151 S HIS
L12            4 S L7 AND (NTIBOD? OR ANTI)
L13            8 S L7 AND (ANTIBOD? OR ANTI)
L14            8 S L13 OR L10
L15            0 S L8 NOT L14

     FILE 'WPIDS' ENTERED AT 09:52:49 ON 29 JUL 1997

     FILE 'WPIDS' ENTERED AT 09:54:32 ON 29 JUL 1997

=> d .wp 1-8 l14

L14  ANSWER 1 OF 8  WPIDS   COPYRIGHT 1997 DERWENT INFORMATION LTD
AN   96-188197 [19]   WPIDS
DNC  C96-060068
TI   Treatment of inflammatory joint disease with C5 blocker -
     which inhibits cell lysing ability of complement complex
     in e.g. rheumatoid arthritis or osteoarthritis.
DC   B05
IN   MATIS, L; WANG, Y
PA   (ALEX-N) ALEXION PHARM INC
CYC  19
PI   WO 9609043  A1 960328 (9619)* EN   70 pp
        RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
         W: AU CA JP
     AU 9537292  A  960409 (9629)
     EP 777474   A1 970611 (9728)  EN
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R: DE ES FR GB NL
ADT WO 9609043 A1 WO 95-US12404 950921; AU 9537292 A AU 95-37292 950921; EP 777474 A1 EP 95-935171 950921, WO 95-US12404 950921
FDT AU 9537292 A Based on WO 9609043; EP 777474 A1 Based on WO 9609043
PRAI US 94-311489 940923
AB WO 9609043 A UPAB: 960510
Treating established joint inflammation in a human or non-human patient comprises administering an **anti**-inflammatory amt. of a **C5** blocker. Also claimed is a pharmaceutical agent contained within packaging material where: (a) the pharmaceutical agent comprises a **C5** blocker which provides the agent with **anti**-inflammatory properties and (b) the packaging material comprises a label which indicates that the pharmaceutical agent is for use in the treatment of joint inflammation and/or of arthritis.
USE - The types of joint inflammation diseases which may be treated are rheumatoid arthritis and juvenile onset rheumatoid arthritis and also osteoarthritis.
ADVANTAGE - Admin. of the **C5** blockers arrests and/or reduces inflammation in joints which are already inflamed and inhibits the spread of inflammation to unaffected joints.
Dwg.5A/10

L14 ANSWER 2 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 95-392923 [50] WPIDS
DNC C95-169278
TI Treating glomerulonephritis with **antibody** against **complement C5** component - to inhibit **complement** induced cell lysis.
DC B04 D16
IN EVANS, M J; MATIS, L; MUELLER, E E; NYE, S H; ROLLINS, S; ROTHER, R P; SPRINGHORN, J P; SQUINTO, S P; THOMAS, T C; WANG, Y; WILKINS, J A
PA (ALEX-N) ALEXION PHARM INC
CYC 15
PI WO 9529697 A1 951109 (9550)* EN 181 pp
AU 9524747 A 951129 (9609)
EP 758904 A1 970226 (9714) EN
R: AT BE CH DE DK ES FR GB IE IT LI NL PT SE
ADT WO 9529697 A1 WO 95-US5688 950501; AU 9524747 A AU 95-24747 950501; EP 758904 A1 EP 95-919041 950501, WO 95-US5688 950501
FDT AU 9524747 A Based on WO 9529697; EP 758904 A1 Based on WO 9529697
PRAI US 94-236208 940502
AB WO 9529697 A UPAB: 951215
Glomerulonephritis (GN) is treated by admin. of an **antibody** (Ab) that binds to **complement** component **C5** in the blood to reduce the cell-lysing activity of **complement**. Also new are: (1) Ab specific for the **alpha chain** of human **C5**, able to inhibit **complement** activated lysis but unable to bind specifically to the free C5a activation product; (3) the hybridoma 5G1.1 (ATCC HB.11625); (4) Abs produced by this hybridoma or **antibodies** able to compete with it for binding to **C5 alpha chain**; (5) a nucleic acid (I) encoding a single chain (sc) Fv polypeptide of 248 amino acids.
USE - The Abs practically eliminate glomerular inflammation and enlargement associated with GN, and can also be used wherever inhibition of **complement** is required, e.g. in cases of inflammatory joint disease or in treatment of immunological or haematological disorders associated with extracorporeal circulation. The isolated **alpha chain** of **C5** and

peptides can be used to induce prodn. of Ab by immunisation, or to screen candidate **antibodies** for **anti-C5** activity.

ADVANTAGE - Ab are specific for **C5** and do not affect opsonic, **anti**-infective and immune complex clearance functions of **complement**. Some Abs block haemolysis by **complement** at close to the theoretical 1:2 **antibody** :antigen ratio.

Dwg.0/19

L14 ANSWER 3 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 95-351129 [45] WPIDS
DNC C95-153772
TI Redn. of immune/haemostatic dysfunction during extracorporeal circulation - by admin. of an **anti-C5** **antibody** to reduce e.g. **complement**, platelet or leukocyte activation and/or platelet-leukocyte adhesion.
DC B04
IN ROLLINS, S A; SMITH, B R; SQUINTO, S P
PA (ALEX-N) ALEXION PHARM INC; (UYYA) UNIV YALE
CYC 6
PI WO 9525540 A1 950928 (9545)* EN 35 pp
AU 9521917 A 951009 (9603)
EP 751787 A1 970108 (9707) EN
R: DE ES FR GB NL
ADT WO 9525540 A1 WO 95-US3614 950322; AU 9521917 A AU 95-21917 950322; EP 751787 A1 EP 95-914820 950322, WO 95-US3614 950322
FDT AU 9521917 A Based on WO 9525540; EP 751787 A1 Based on WO 9525540
PRAI US 94-217391 940323
AB WO 9525540 A UPAB: 951114
The following are claimed:(A) a method for performing a therapeutic procedure on a patient, which comprises:(a) passing circulating blood from a blood vessel of the patient through a conduit (which has a luminal surface comprising a material capable of causing **complement** activation (CA), platelet activation (PA), leukocyte activation (LA) and/or platelet-leukocyte adhesion (PLA) in the patient's blood) and back to a blood vessel of the patient, and(b) introducing an **antibody** which specifically binds to **complement** component **C5**, into the patient's bloodstream, in an amt. effective to reduce CA, PA, LA and/or PLA resulting from passage of the circulating blood through the conduit; step (a) occurs before, during and/or after step (b);(B) an article of manufacture comprising packaging material and a pharmaceutical agent contained within the packaging material, where:(a) the pharmaceutical agent comprises an **antibody** as above, and(b) the packaging material comprises a label which indicates that the pharmaceutical agent is for use with an extracorporeal circulation procedure.

USE - The method can be used to perform a cardiopulmonary bypass procedure (claimed). More generally, the process may be used to reduce dysfunction of the immune and haemostatic systems, associated with extracorporeal circulation (ECC). These include e.g. the development of inflammation, platelet dysfunction and thrombocytopenia.

ADVANTAGE - No further details.

Dwg.0/4

L14 ANSWER 4 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 95-139556 [18] WPIDS

DNC C95-064463
TI Chimeric proteins which inhibit **complement** activation - useful for the treatment of **complement** mediated inflammation and auto immune diseases..
DC B04 D16
IN HIGGINS, P J; KO, J; YEH, C G
PA (CYTO-N) CYTOMED INC
CYC 21
PI WO 9508570 A1 950330 (9518)* EN 74 pp
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: AU CA CN JP
AU 9480719 A 950410 (9530)
EP 723555 A1 960731 (9635) EN
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
JP 09502985 W 970325 (9722) 62 pp
ADT WO 9508570 A1 WO 94-US10786 940923; AU 9480719 A AU 94-80719 940923; EP 723555 A1 EP 94-931763 940923, WO 94-US10786 940923; JP 09502985 W WO 94-US10786 940923, JP 95-509957 940923
FDT AU 9480719 A Based on WO 9508570; EP 723555 A1 Based on WO 9508570; JP 09502985 W Based on WO 9508570
PRAI US 93-126596 930924; US 94-310416 940922
AB WO 9508570 A UPAB: 950518
A chimeric protein (CP) is claimed which comprises a first polypeptide (PP1) which inhibits **complement** activation, linked to a second polypeptide (PP2) which inhibits **complement** activation, where PP1 and PP2 can be the same or different. Also claimed are: (1) a nucleic acid encoding a CP where PP1 and PP2 are linked by a peptide bond; (2) a recombinant expression vector comprising a selectable marker and the nucleic acid of (1) operably linked to regulatory sequences for the expression of the CP; (3) a process for preparing a recombinant CP comprising culturing a suitable host cell comprising the vector of (2) under conditions promoting expression; (4) a method of inhibiting C3a and C5a generation comprising: (a) contacting a C3 convertase with the CP; (b) contacting a **C5** convertase with the CP, where binding of the CP with the C3 convertase and **C5** convertase inhibits the generation of C3a and C5a respectively; and (5) an **antibody** which binds to the soluble CP but does not bind to PP1 or PP2 alone.
USE - The CPs may be used for reducing inflammation characterised by excessive **complement** activation (claimed). The CPs may also be used in the treatment of autoimmune diseases. Monoclonal **antibodies** directed against the CPs may be used as diagnostic or therapeutic agents. The CPs can be combined with an appropriate pharmaceutical formulation and administered by a variety of routes including intravenous bolus injection, intravenous infusion, intraperitoneal, intradermal, intramuscular, subcutaneous, intranasal and oral routes.
Dwg.0/15

L14 ANSWER 5 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 91-038259 [06] WPIDS
DNN N91-029558 DNC C91-016357
TI Sensitive assay of C5a **complement** peptide - by reaction with immobilised specific **antibody**, detectable **antibody**, and monoclonal **antibodies**, for treating sepsis, etc..
DC B04 D16 J04 S03
IN GOTZE, O; OPPERMANN, M; SCHULZE, M

PA (GOTZ-I) GOTZE O
CYC 9
PI EP 411306 A 910206 (9106)*
R: BE CH DE FR GB IT LI NL SE
DE 3924924 A 910207 (9107)
ADT EP 411306 A EP 90-111920 900622; DE 3924924 A DE 89-3924924 890727
PRAI DE 89-3924924 890727
AB EP 411306 A UPAB: 930928
Detection and/or quantitative determination of the **complement** peptides C5a and/or C5a-des-Arg (C5a') in biological fluid comprises: (1) contacting test sample with a matrix to which **antibodies** (Ab1), able to bind C5a and/or C5a' are fixed; (2) contacting the incubated matric with second detectable **antibodies** (Ab2), or their fragments, which bind to native **C5**, C5a and/or C5a' and (3) detecting Ab2 or its fragments. Also new are (1) test kits for this process; (2) cell lines producing monoclonal **antibodies** (MAb) which bind, in C5a and C5a' to the receptor binding site for the C5a-specific receptors, but not with the corresponding amino acid sequenc in native **C5**; (3) MAb produced by these cell lines, (4) **anti**-idiotypic **antibodies** (AIAb) against MAb produced by the specified cell lines, and (5) the cell line CNCM I-188 which produces the AIAb F23/14.
USE/ADVANTAGE - This method provides reliable and sensitive assay of C5a and C5a' with detection sensitivity 20 pg/ml (compare 1 ng/ml for the known process), allowing C5a to be assayed in normal plasma samples. Compsns. contg. MAb can be used to treat and prevent diseases associated with elevated C5a levels in the blood (esp. adult respiratory distress syndrome, sepsis, shock) or other disorders related to intra- or extra-vascular **complement** activation (e.g. rheumatic polyarthritis or lupus erythematosus). AIAb can be used to block reaction of C5a with its receptors.
2/10

L14 ANSWER 6 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 89-309498 [42] WPIDS
CR 91-132854 [18]; 93-175454 [21]
DNC C89-137014
TI New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of **complement** related immune defects, inflammation, myocardial infarct, etc..
DC B04 D16
IN CARSON, G R; CONCINO, M F; FEARON, D T; IP, S H; KLICKSTEIN, L B; MAKRIDES, S C; MARSH, H C; WONG, W W
PA (BGHM) BRIGHAM & WOMENS HOSPITAL; (TCEL-N) T CELL SCI INC; (UYJO) UNIV JOHNS HOPKINS
CYC 20
PI WO 8909220 A 891005 (8942)* EN 191 pp
RW: AT BE CH DE FR GB IT LU NL SE
W: AU DK FI JP KR NO SU
ZA 8902397 A 891129 (9002)
AU 8935394 A 891016 (9008)
CN 1036987 A 891108 (9033)
ES 2014593 A 900716 (9033)
FI 9004842 A 901001 (9105)
EP 411031 A 910206 (9106)
R: AT BE CH DE FR GB IT LU NL SE
NO 9004213 A 901109 (9106)
DK 9002348 A 901130 (9113)

JP 04501502 W 920319 (9218) 59 pp
AU 647371 B 940324 (9417)
EP 411031 A4 920205 (9520)
ADT WO 8909220 A WO 89-US1358 890331; ZA 8902397 A ZA 89-2397 890331; ES 2014593 A ES 89-112 890331; EP 411031 A EP 89-905249 890331; JP 04501502 W JP 89-505000 890331; AU 647371 B AU 89-35394 890331; EP 411031 A4 EP 89-905249 890331
FDT AU 647371 B Previous Publ. AU 8935394, Based on WO 8909220
PRAI US 88-176532 880401
AB WO 8909220 A UPAB: 940622
Nucleic acid sequences encoding a full-length CR1 protein (i.e. the C3b/C4b receptor) is new. The complete sequence over 6000 bases) is reproduced in the specification. Also new are (1) shortened forms of this sequence (specifically lacking the transmembrane region); (2) recombinant vectors and cells contg. such sequences, and (3) proteins (structures reproduced) and their fragments encoded by these sequences.

Pref. the sequence may be DNA or RNA, and can be expressed in bacteria or mammalian cells.

USE - The proteins (or their fragments) bind (3b and/or C4b; have I-cofactor activity and inhibit activity of C3 and **C5** convertases. They are thus useful for treating immune disorders associated with **complement** activity; for preventing or treating damage caused by myocardial infarct or inflammation, and to prevent perfusion injury. The proteins derived **antibodies** and gene sequences can also be used to diagnose such conditions. Dwg.0/31

L14 ANSWER 7 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 87-322653 [46] WPIDS
DNN N87-241265 DNC C87-137507
TI Mono clonal **antibodies** against C5A or DES-ARG74-C5A **complement** - used for treating injurious intravascular **complement** activation conditions or in diagnosis.
DC B04 D16 S03
IN DEINHART, T E; FENDLY, B M; LARRICK, J W
PA (CETU) CETUS CORP; (CETU) CETUS ONCOLOGY CORP
CYC 14
PI EP 245993 A 871119 (8746)* EN 14 pp
R: AT BE CH DE ES FR GB GR IT LI LU NL SE
JP 62269699 A 871124 (8801)
EP 245993 B1 930526 (9321) EN 18 pp
R: AT BE CH DE ES FR GB GR IT LI LU NL SE
DE 3785967 G 930701 (9327)
ES 2054667 T3 940816 (9434)
ADT EP 245993 A EP 87-303762 870428; JP 62269699 A JP 87-103396 870428; EP 245993 B1 EP 87-303762 870428; DE 3785967 G DE 87-3785967 870428, EP 87-303762 870428; ES 2054667 T3 EP 87-303762 870428
FDT DE 3785967 G Based on EP 245993; ES 2054667 T3 Based on EP 245993
PRAI US 86-856780 860428; US 86-947839 861230
AB EP 245993 A UPAB: 930922
A novel monoclonal **antibody** (MAb) binds with an affinity of at least 10 power 8 l/mole to human **complement** component C5a or des-arg74-C5a in the presence or absence of a molar excess of **complement** component **C5** and blocks the binding of human C5a or human des-arg74-C5a to human granulocytes.

USE - The **antibody** blocks the effect of C5a or des-arg74-C5a in vivo. It is used for prophylactically or therapeutically treating a patient for a condition associated with

injurious intravascular **complement** activation including patients receiving immunosuppressive therapy and those suffering from severe thermal burns or other serious injuries. Such conditions include Gram-negative sepsis, ARDS, thermal injury, pulmonary inflammation or injury, severe trauma, pancreatitis, myocardial infarction, massive blood transfusion, blood clots, cardiovascular disease, exposure to medical devices and/or acute phases of chronic autoimmune disease (including systemic lupus erythrematosus and rheumatoid arthritis). The MAbs may also be used immunologically or immunodiagnostically to detect the presence of human C5a or human des-arg74-C5a in fluids. The specificity of the MAbs renders them useful for immunological studies of human C5a and its des-arg deriv., for affinity purifcn. of C5a or des-arg74-C5a and for neutralisation and/or removal of C5a or des-arg74-C5a from any reagents where it might be present.
0/0

L14 ANSWER 8 OF 8 WPIDS COPYRIGHT 1997 DERWENT INFORMATION LTD
AN 84-006966 [02] WPIDS
DNN N84-005116 DNC C84-002802
TI Removal of **complement** components from biological fluids - by treatment with buffered acrinol to leave soln. for fragment assay.
DC B04 K08 S03
IN SATOH, P S
PA (UPJO) UPJOHN CO
CYC 12
PI EP 97440 A 840104 (8402)* EN 14 pp
R: BE CH DE FR GB IT LI NL SE
JP 59005958 A 840112 (8408)
FI 8302120 A 840131 (8411)
CA 1202235 A 860325 (8617)
EP 97440 B 860924 (8639) EN
R: BE CH DE FR GB IT LI NL SE
DE 3366421 G 861030 (8645)
JP 04069345 B 921105 (9249) 6 pp
ADT EP 97440 A EP 83-303142 830601; JP 59005958 A JP 83-104846 830610; JP 04069345 B JP 83-104846 830610
FDT JP 04069345 B Based on JP 59005958
PRAI US 82-388068 820614; US 83-518603 830729
AB EP 97440 A UPAB: 930925
Removal of **complement** components C3, C4 and **C5** from a biological fluid sample and recovery from the fluid of fragments C3a, C4a and C5a or their des-Arg derivs. is effected by adding an equal vol. of buffered 0.8-1.6% acrinol soln. to the sample, incubating the mixt. for 1 min.-2 hrs. at 25 deg.C and recovering the supernatant contg. the desired fragments.

In an assay for the fragments or their des-Arg derivs. the supernatant is then incubated with a known amount of **antibody** recognising the fragment or des-Arg deriv. The free labelled fragment is sepd. from the bound labelled fragment and the amount of labelled fragment in either material is measured. The results are compared with a standard curve.

The **complement** components are removed from biological samples, e.g. plasma, serum or urine, while fragments C3a, C4a and C5a and their des-Arg derivs. are recovered without interference with their immunogenicity. The fragments are anaphylatoxins and are involved in acute inflammatory processes, and so their assay is useful in medical diagnosis, esp. in the detection of autoimmune

disorders and of iatrogenic **complement** activation.
0/0

=> fil biosis
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FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 26 July 1997 (970726/ED)
CAS REGISTRY NUMBERS (R) LAST ADDED: 26 July 1997 (970726/UP)

=> d que l6;d his l7-
L1 737 SEA FILE=BIOSIS ABB=ON "EVANS M"/AU OR "EVANS M J"/AU
L2 138 SEA FILE=BIOSIS ABB=ON ("MATIS L"/AU OR "MATIS L A"/AU)

L3 666 SEA FILE=BIOSIS ABB=ON "MUELLER E"/AU OR "MUELLER E E"/A
U
L4 17 SEA FILE=BIOSIS ABB=ON ("NYE S"/AU OR "NYE S H"/AU)
L5 81 SEA FILE=BIOSIS ABB=ON ("ROLLINS S"/AU OR "ROLLINS S A"/
AU OR "ROLLINS S B"/AU OR "ROLLINS S D"/AU OR "ROLLINS S
L"/AU OR "ROLLINS S M"/AU OR "ROLLINS S R"/AU)
L6 1605 SEA FILE=BIOSIS ABB=ON L1 OR L2 OR L3 OR L4 OR L5

(FILE 'BIOSIS' ENTERED AT 09:55:17 ON 29 JUL 1997)
L7 1476 S COMPLEMENT AND C5
L8 14 S L7 AND L6
L9 10288 S ALPHA (2W) CHAIN#
L10 64 S L7 AND L9
L11 391924 S ANTIBOD? OR ANTI (2A) C5
L12 13 S L10 AND L11
~~L13 14 S L8 NOT L12~~
L14 14 S L8 NOT L12

FILE 'BIOSIS' ENTERED AT 09:58:09 ON 29 JUL 1997

=> d bib ab l12 1-13;d bib ab l14 1-14

L12 ANSWER 1 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 93:143342 BIOSIS
DN BA95:76142
TI MOLECULAR BASIS OF **COMPLEMENT** RESISTANCE OF HUMAN MELANOMA
CELLS EXPRESSING THE C3-CLEAVING MEMBRANE PROTEASE P65.
AU OLLERT M W; KADLEC J V; PETRELLA E C; BREDEHORST R; VOGEL C-W
CS DEP. BIOCHEM. MOLECULAR BIOL., UNIV. HAMBURG, MARTIN-LUTHER-KING-PL.
6, 2000 HAMBURG 13, GER.
SO CANCER RES 53 (3). 1993. 592-599. CODEN: CNREA8 ISSN: 0008-5472
LA English
AB The molecular mechanism of **complement** resistance of the
human SK-MEL-170 melanoma cell line was investigated. The cells have
been shown to express the C3b-cleaving membrane protease p65. To
delineate the molecular consequences of the C3b-cleaving activity for
the **complement** cytotoxicity, the molecular events during
the initiation (R24 monoclonal **antibody**, C1), amplification

(C4, C3), and membrane attack (**C5**, C9) phases of **complement** were studied in comparison to a **complement**-susceptible human melanoma line (SK-MEL-93-2). No cleavage of C4b and C5b, 2 molecules structurally similar to C3b, was observed on the cells during classical pathway activation indicating the specificity of the p65 protease for the C3b molecule. The rapid degradation of C3b by p65 on the surface of **complement**-resistant SK-MEL-170 cells generates a Mr 30,000 C3.**alpha**.'-**chain**-fragment detectable as early as 1 min after **complement** activation, whereas no such fragment was present in detectable amounts on **complement**-susceptible cells. As a result of the rapid C3b proteolysis by p65 on resistant SK-MEL-170 cells, less **C5** convertases are formed, which in turn results in the formation of a lower number of terminal **complement** components and membrane attack complexes. R24 **antibody** and C1q binding to the resistant cells was slightly lower as to susceptible cells. C4 binding studies, however, revealed that the observed difference in **antibody** and C1q binding has no influence on the **complement** resistance of SK-MEL-170 cells: significantly more C4b was bound to **complement**-resistant (1565 .+-. 92 fg/cell) as compared to susceptible cells (715 .+-. 31 fg/cell). On extraction of the molecular forms of C4 bound to the cell membranes, an additional high molecular weight C4 species-apparently a C4b-C4b homodimer-appeared only on the resistant SK-MEL-170 cells that may function as a residual back-up **C5** convertase. Collectively, these results show that SK-MEL-170 human melanoma cells evade **complement**-mediated cytolysis despite sufficient activation of early components of the classical **complement** pathway by p65-mediated rapid degradation of surface-bound C3b, leading to a significant reduction in membrane attack complex formation. Thus, rapid cleavage of surface deposited C3b was established as a powerful mechanism of **complement** resistance.

L12 ANSWER 2 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 92:477083 BIOSIS
DN BA94:108458
TI FORMATION AND STRUCTURE OF THE C5B-7 COMPLEX OF THE LYTIC PATHWAY OF **COMPLEMENT**.
AU DISCIPIO R G
CS DEP. IMMUNOLOGY IMM18, RESEARCH INSTITUTE SCRIPPS CLINIC, 10666 N. TORREY PINES RD., LA JOLLA, CALIF. 92037.
SO J BIOL CHEM 267 (24). 1992. 17087-17094. CODEN: JBCHA3 ISSN: 0021-9258
LA English
AB The formation and structure of the **complement** cytolytic intermediary complex, C5b-7, were studied with the aim of determining the interactive regions of **C5**, C6, and C7. The structure of human **complement** component **C5** was elucidated by the application of limited proteolysis which generated well characterized major polypeptide fragments of this molecule. Plasmin, thrombin, and kallikrein cleave C5b with greater facility than **C5**. The most useful cleavage of C5b was effected by plasmin because the fragmentation pattern was similar to the processing the C3b by factors H, I, and kallikrein. Plasmin hydrolyzes peptide bonds within the .**alpha**.'-**chain** of C5b, resulting in a four-chain fragment, C5c (Mr = 142,000), and a single chain fragment, C5d (Mr = 43,000). Circular dichroism spectroscopic analyses indicated that C5d is substantially richer in .alpha.-helical content

than is C5c (27 versus 9%). Polyclonal **antibodies** directed against C5c blocked the interaction of C5b-6 with C7, whereas **antibodies** directed against C5d inhibited the binding of **C5** with C3b. Chemical cross-linking using a cleavable radioiodinated photoreactive reagent revealed that both C6 and C7 associate preferentially with the .**alpha**.'-**chain** of C5b. The reversible interactions of **C5** with C6, C7, and major polypeptide fragments derived from these were investigated with solid phase binding assays. The results indicate that the carboxyl-terminal domains of C6 and C7, which have cysteine-rich modules homologous to those found in factors H and I, have the capacity to link specifically with **C5**.

L12 ANSWER 3 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 92:28069 BIOSIS
DN BA93:17344
TI AMINO ACID RESIDUES 1101-1105 OF THE ISOTYPIC REGION OF HUMAN C4B IS IMPORTANT TO THE COVALENT BINDING ACTIVITY OF **COMPLEMENT** COMPONENT C4.
AU REILLY B D; LEVINE R P; SKANES V M
CS FACULTY MEDICINE, MEMORIAL UNIVERSITY NEWFOUNDLAND, ST. JOHN'S, NFLD. CAN. A18 3V6.
SO J IMMUNOL 147 (9). 1991. 3018-3023. CODEN: JOIMA3 ISSN: 0022-1767
LA English
AB The C4A and C4B isotypes of human C4 show certain functional differences that stem from their relative preference for transacylation to amino (-NH2) vs hydroxyl (-OH) nucleophiles, respectively, on **complement**-activating surfaces. Comparison of amino acid sequences of the .**alpha**.-**chain** fragment of C4, C4d, has shown C4A- and C4B-specific sequences at residues 1101-1106 are the only consistent structural difference between isotype, i.e., Pro, Cys, Pro, Val, Leu, Asp in C4A and Leu, Ser, Pro, Val, Ile, His in C4B. These residues may be responsible either in part or entirely for properties associated with isotype. To examine the functional role of residues 1101-1106 in C4B-mediated hemolysis, whole serum or immunopurified human C4 with allotypes, A3B1, A3, B2B1, or B1 were preincubated in the presence or absence of an antipeptide mAb (BII-1) specific for amino acid residues 1101-1105 of C4B. Sensitized sheep E and C4-deficient guinea pig serum was then added and lysis measured by absorbance at 415 nm. Our results show lysis of **antibody**-sensitized sheep E is inhibited by **antibody** and C4B2B1, C4B1, or C4A3B1 but not **antibody** and C4A3. The interference of hemolysis by BII-1 could not be explained by inhibition of activation of C4B or inhibition of C3 or **C5** convertase activity. Furthermore, results from uptake experiments show that BII-1 interferes with the covalent binding activity of C4B, indicating residues 1101-1105 play a role in the covalent binding reaction of C4B to the target E-**antibody** complex.

L12 ANSWER 4 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 91:409305 BIOSIS
DN BA92:76270
TI A COVALENT DIMER OF **COMPLEMENT** C4B SERVES AS A SUBUNIT OF A NOVEL **C5** CONVERTASE THAT INVOLVES NO C3 DERIVATIVES.
AU MASAKI T; MATSUMOTO M; YASUDA R; LEVINE R P; KITAMURA H; SEYA T
CS DEP. IMMUNOLOGY, CENTER ADULT DISEASES, OSAKA, HIGASHINARI-KU, OSAKA 537, JPN.
SO J IMMUNOL 147 (3). 1991. 927-932. CODEN: JOIMA3 ISSN: 0022-1767

LA English
AB A C intermediate, LAC14, was prepared from TNP-aminocaproyl liposomes sensitized with anti-TNP **antibody** (Ab) and purified human C1 and C4. LAC14, containing radiolabeled C4, was analyzed by SDS-PAGE followed by autoradiography, and yielded a 210-kDa band and a predominant 400-kDa band. The 210-kDa band consisted of monomeric C4b bound to low molecular mass acceptors. The 400-kDa band was comprised of a 200-kDa moiety, as well as .beta.- and .gamma.-chains of C4. The 200-kDa moiety contained neither C1 nor sensitizing Ab, but it was largely decreased by treatment with NH2OH to the 90-kDa moiety with the mobility corresponding to the .**alpha**.'-**chain** of C4b. A covalent dimer of C4b, therefore, is the predominant form of C4b deposited on liposomes sensitized with **antibody**. The C4b-C4b dimer formed rapidly (within 5 min) followed by slow dissociation into monomers. The LAC14 bearing the C4b dimer but not the monomer was lysed, although with relatively low efficiency, by the addition of oxyC2 and EDTA-supplemented C3-deficient serum (C3DS), and, furthermore, LAC142 possessed the ability to convert **C5** into C5a and C5b. Moreover, lysis was inhibited not by anti-C3 Ab but by anti-C4 Ab. In other experiments, the dimer served as an element of C3 convertase, as well. These findings imply that the C4b dimer, when complexed with C2, expresses C3/**C5** convertase activity without participation of C3, and may provide a molecular mechanism whereby sera from patients with complete C3 deficiency retain the ability to induce C-mediated cytolysis.

L12 ANSWER 5 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 89:448305 BIOSIS
DN BA88:96577
TI RAPID ISOLATION AND CHARACTERIZATION OF NATIVE MOUSE **COMPLEMENT** COMPONENTS C3 AND **C5**.
AU VAN DEN BERG C W; VAN DIJK H; CAPEL P J A
CS ACADEMIC HOSP. UTRECHT, LAB. MICROBIOL., POSTBUS 85500, 3508 GA UTRECHT, NETHERLANDS.
SO J IMMUNOL METHODS 122 (1). 1989. 73-78. CODEN: JIMMBG ISSN: 0022-1759
LA English
AB A rapid, 1 day procedure for the purification of mouse **complement** factors C3 and **C5** is described. The method is based on fractionated precipitation by polyethylene glycol 6000, followed by MonoQ anion exchange chromatography on a system for fast protein liquid chromatography (FPLC). For C3 isolation, an additional FPLC separation step using Superose 12 (gel filtration) was used. C3 was purified 71-fold with a yield of 32% as measured by biological activity; the preparation contained no detectable contaminants as judged by SDS-PAGE. A comparable procedure for the isolation of **C5** resulted in a preparation with a considerable contamination which could be easily removed by affinity chromatography using **antibodies** directed against these contaminants. With this combined procedure **C5** was purified 536-fold with a yield of 28% based on biological activity. SDS-polyacrylamide gel electrophoresis revealed that mouse C3 and **C5** had apparent Mrs of 170,000 and 190,000, respectively. Under reducing conditions the .**alpha**. and .beta. **chains** showed Mrs of 107,000 and 62,000 for C3, and 104,000 and 85,000 for **C5**.

L12 ANSWER 6 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS

AN 88:482712 BIOSIS
DN BA86:114022
TI ANALYSIS OF HUMAN C8 WITH MONOCLONAL **ANTIBODIES** CHARACTERIZATION OF A MONOCLONAL **ANTIBODY** THAT RECOGNIZES FREE C8-ALPHA-GAMMA SUBUNIT.
AU DOGLIO L T; GAWRYL M S; LINT T F
CS DEP. IMMUNOL./MICROBIOL., RUSH-PRESBYTERIAN-ST. LUKE'S MED. CENT., CHICAGO, ILLINOIS 60612.
SO J IMMUNOL 141 (6). 1988. 2079-2083. CODEN: JOIMA3 ISSN: 0022-1767
LA English
AB The eighth component of human C is essential for the formation of the membranolytic C attack complex. C8 has a unique structure in that two covalently linked chains, C8.alpha. and C8.gamma., are associated non-covalently with the third chain, C8.beta.. In order to study the structure and assembly of the C8 molecule, a panel of mAb has been produced against the C component C8. Eight of these mAb had reactivity to the C8.alpha.-.gamma. subunit, whereas four reacted with C8.beta.. One of the C8.alpha.-.gamma. mAb, C8A2, had specificity for an epitope on the C8.**alpha**.-**chain** and exhibited no cross-reactivity to any of the other terminal C components, including C8.beta.. C8A2 inhibited the hemolytic activity of the C8.alpha.-.gamma. subunit but had no effect on the activity of fluid phase whole C8 or C8 within membrane-bound C5b8. Functional experiments suggest that C8A2 inhibits C8.alpha.-.gamma. activity by interfering with its interaction with the C8.beta.-chain. In an enzyme immunoassay using the C8A2 mAb, free C8.alpha.-.gamma. subunit could be detected in both homozygous and heterozygous C8.beta.-deficient serum. However, only low level binding was observed when homozygous **C5**- and C7-deficient sera were tested. Thus the mAb, C8A2, recognizes an epitope expressed on the C8.alpha.-.gamma. subunit but not on intact C8 and can detect free C8.alpha.-.gamma. in the presence of native C8.

L12 ANSWER 7 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 88:331418 BIOSIS
DN BA86:37969
TI USE OF ANTISERA TO THE ISOLATED ALPHA AND BETA SUBUNITS OF C3 AS PROBES TO STUDY FUNCTIONAL SITES PRESENT ON PARTICLE-BOUND C3B BUT ABSENT ON NATIVE SOLUBLE FORMS OF C3.
AU WHALEY K; NILSSON U
CS BLOOD CENTRE, UNIV. HOSP., S-751 85 UPPSALA, SWEDEN.
SO INT ARCH ALLERGY APPL IMMUNOL 86 (1). 1988. 55-61. CODEN: IAAAAM ISSN: 0020-5915
LA English
AB The effect of antisera to the isolated .**alpha**. and .beta. **chains** of C3 on certain C3b-dependent reactions has been studied. **C5**-mediated haemolysis of EAC1423b was inhibited preferentially by antiserum to the .**alpha**. **chain**, whereas antiserum to the .beta. chain inhibited the formation of C3bBb. The anti-.beta. chain antiserum also stabilised C3bBbP, and rendered the enzyme relatively resistant to accelerated decay in the presence of factor H. These and previous findings that anti-.alpha. and anti-.beta. IgG bind to restricted subsets of antigenic determinants on C3/C3b suggest that these antisera affect C3b function through the binding of **antibodies** to active binding sites exclusively exposed by bound C3b. The anti-.alpha. and anti-.beta. **antibody** probes are currently being further developed to verify this interpretation.

L12 ANSWER 8 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 87:359289 BIOSIS
DN BA84:56692
TI TRYPANOSOMA-LEWISI RESTRICTION OF ALTERNATIVE **COMPLEMENT** PATHWAY C3-**C5** CONVERTASE ACTIVITY.
AU STURTEVANT J E; BALBER A E
CS DIV. IMMUNOL., DEP. MICROBIOL. AND IMMUNOL., DUKE UNIVERSITY MED. CENT., P.O. BOX 3010, DURHAM, N.C. 27710, USA.
SO EXP PARASITOL 63 (3). 1987. 260-271. CODEN: EXPAAA ISSN: 0014-4894
LA English
AB The rat parasite Trypanosoma lewisi was incubated in vitro with rat or human serum, washed, and extracted in detergent. Extracts were fractionated by electrophoresis in denaturing gels, transferred to nitrocellulose, allowed to renature, then immunoblotted with polyclonal **antibodies** to rat **complement** component C3 and human **complement** components C3, **C5**, and factor B. Molecules that reacted with these **antibodies** were detected in the extracts. Fragments of rat C3 were detected in extracts of parasites that had not been exposed to serum in vitro. Additional **complement** deposition occurred during in vitro incubations; human **complement** components deposited in vitro could be distinguished from rat components deposited in vivo. **Complement** deposition in vitro required magnesium ions and did not occur when heat inactivated serum was used. Components reacting with **antibodies** to human C3 included a group of bands with molecular weights higher than C3.**alpha**. or .beta. **chains**. Blotting with affinity purified, chain specific **antibodies** demonstrated that a 68 kDa component on parasites is C3.beta. and that a 44 kDa molecule is derived from C3.alpha.. A 73 kDa component that was difficult to resolve from C3.beta. is probably also a C3.alpha. fragment. This suggests that an inactive iC3b-like molecule is present on parasites. Kinetic studies showed that cleavage of C3.alpha. is rapid and that the amount of C3.alpha. fragments and C3.beta. on intact parasites reached a steady state after 15 min. When parasites were trypsinized prior to incubation in **C5** or C6 deficient serum, the rate and extent of C3 and **C5** deposition increased. Unprocessed C3.alpha.' and **C5**.**alpha**.' **chains** were detected. Trypsinized parasites were lysed by the alternative **complement** pathway in normal serum. Intact parasites could be lysed by **complement** in the presence of **antibody**. The data support our previous suggestion that trypsin sensitive surface proteins on intact T. lewisi limit alternative pathway activity by restricting C3/**C5** convertase activity.

L12 ANSWER 9 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 87:337772 BIOSIS
DN BA84:46715
TI FUNCTIONAL ANALYSIS AND QUANTIFICATION OF THE **COMPLEMENT** C3 DERIVED ANAPHYLATOXIN C3A WITH A MONOCLONAL **ANTIBODY**.
AU BURGER R; BADER A; KIRSCHFINK M; ROTHER U; SCHROD L; WOERNER I; ZILOW G
CS INST. IMMUNOL., IM NEUENHEIMER FELD 305, 6900 HEIDELBERG, W. GER.
SO CLIN EXP IMMUNOL 68 (3). 1987. 703-711. CODEN: CEXIAL ISSN: 0009-9104
LA English
AB The C3 fragment C3a belongs to the anaphylatoxins. It has immune regulatory activity and contributes to the pathogenesis of the adult respiratory distress syndrome (ARDS). The low molecular weight (9 kD)

of C3a complicates the production of **antibodies** to C3a. We obtained a monoclonal **antibody** (designated H13) to human C3a. It reacts with C3a or C3a-desArg and with native C3 but not with **C5** or C5a. In immunoblot analysis it reacts with the .alpha.- but not with .beta.-chain of C3 and binds to a protein with a mol. wt of about 10 kD present in zymosan-activated sera which is only marginally detectable in non-activated serum and absent in plasma. H13 crossreacts with the analogous proteins of rabbit, guinea pig and sheep. H13 has the capacity to bind 125I-radiolabelled C3a efficiently but fails totally to react with 125I-C5a or with other C3 .**alpha**.-**chain** fragments, H13 blocks C3a functional activity. It markedly inhibits C3a-induced 3H-serotonin release from platelets in vitro and similarly inhibits the C3a-induced extravasation of Evans blue into the skin in vivo. H13 does not interfere with the haemolytic activity of C3. An ELISA system was established using H13 which permits quantification of C3a in sera of polytrauma patients. The **antibody** H13 should facilitate further functional analysis of C3a in experimental systems. It should be useful for quantification of C3a in diagnostic assays and also for application in immunopathology.

L12 ANSWER 10 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 87:337585 BIOSIS
DN BA84:46528
TI COVALENT ASSOCIATION OF C3B WITH C4B WITHIN **C5** CONVERTASE OF THE CLASSICAL **COMPLEMENT** PATHWAY.
AU TAKATA Y; KINOSHITA T; KOZONO H; TAKEDA J; TANAKA E; HONG K; INOUE K
CS DEP. BACTERIOLOGY, OSAKA UNIV. MED. SCH., SUITA, OSAKA 565, JAPAN.
SO J EXP MED 165 (6). 1987. 1494-1507. CODEN: JEMEAV ISSN: 0022-1007
LA English
AB The C convertase of the classical **complement** pathway is a complex enzyme consisting of three **complement** fragments, C4b, C2a, and C3b. Previous studies have elucidated functional roles of each subunit (4, 6, 7), but, little is known about how the subunits associate with each other. In this investigation, we studied the nature of the classical C% convertase that was assembled on sheep erythrocytes. We found that one of the nascent C3b molecule that had been generated by the C3 convertase directly bound covalently to C4b. C3b bound to the .**alpha**.' **chain** of C4b through an ester bond, which could be cleaved by treatment with hydroxylamine. The ester bond was rather unstable, with a half-life of 7.9 h at pH 7.4 and 37% C. Formation of the C4b-C3b dimer is quiet efficient; e.g., 54% of the cell-bound C3b was associated with C4b when 25,000 molecules of C4b and 12,000 molecules of C3b were present per cell. Kinetic analysis also showed the efficient formation of the C4b-C3b dimer; the rate of dimer formation was similar to or even faster than that of cell-bound monomeric C3b molecules. These results indicate that the C4b is a highly reactive acceptor molecule for nascent C3b. High-affinity **C5**-binding site with an association constant of 2.1 .times. 108 L/M were demonstrated on C4b-C3b dimer-bearing sheep erthocytes, EAC43 cells. The number of high-affinity **C5**-binding sites coincided with the number of C4b-C3b dimers, but not with the total number of cell-bound C3b molecules. Anti-C4 **antibodies** caused 80% inhibition of the binding of **C5** to EAC43 cells. These results suggest that only C4b-associated C3b serves as a high-affinity **C5** binding site. EAC14 cells had a small amount of high-affinity **C5** binding sites with an association constant of 8.1 .times. 107 L/M 100 molecules of bound C4b being necessary for 1 binding

site. In accordance with the hypothesis that C4b-associated C4b might also serve as a high-affinity **C5**-binding site, a small amount of C4b-C4b dimer was detected on EAC14 cells by SDS-PAE analysis. Taken together, these observations indicate that high-affinity binding of **C5** is probably divalent, in that **C5** recognizes both promoters with dimers. The high-affinity binding may allow selective binding of **C5** to the convertase in spite of surrounding monomeric C3b molecules.

L12 ANSWER 11 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 84:339305 BIOSIS
DN BA78:75785
TI RESIDUAL HEMOLYTIC AND PROTEOLYTIC ACTIVITY EXPRESSED BY BB AFTER DECAY DISSOCIATION OF C-3B BB.
AU FISHELSON Z; MULLER-EBERHARD H J
CS DEPARTMENT OF IMMUNOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, LA JOLLA, CALIF. 92037.
SO J IMMUNOL 132 (3). 1984. 1425-1429. CODEN: JOIMA3 ISSN: 0022-1767
LA English
AB Bb [factor B, fragment b] (MW = 63,000) is the catalytic site-bearing subunit of the C3 [**complement** component 3] convertase of the alternative **complement** pathway, C3b,Bb, which is dissociated from the complex upon decay of the enzyme. Because purified Bb induced certain leukocyte activities, it was examined whether it expresses residual hemolytic or proteolytic activity. Hemolytic activity of Bb was tested by using Factor B- or Factor D-depleted normal human serum and rabbit or sheep erythrocytes. Proteolytic activity of Bb was assessed by using purified C3 or **C5** as substrates and SDS-PAGE [sodium dodecyl sulfate-polyacrylamide gel electrophoresis] to detect protein cleavage. Bb expressed metal-dependent hemolytic activity that was .apprx. 100-fold lower than that of Factor B. This activity could be inhibited by Factor H and enhanced by properdin. Low but statistically significant binding of 125I-labeled Bb to C3b on erythrocytes was demonstrated. Monoclonal **antibodies** that bind to Bb but not to intact Factor B inhibited the Bb hemolytic activity. Purified Bb cleaved C3 to C3a and C3b, as evidenced by the appearance of the .**alpha**.'-**chain** of C3b. It also cleaved **C5** to C5a and C5b when cobra venom factor [CVF] was present in the reaction mixture. Metal ions were required for expression of proteolytic activity, and Ni supported the activity better than Mg. Decayed Bb has residual C3 and **C5** cleaving activity and hemolytic activity, expression of which appears to require its association with C3b, C3(H2O), or CVF. These observations may aid in explaining the mechanism of action of Bb on leukocytes.

L12 ANSWER 12 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 82:150280 BIOSIS
DN BA73:10264
TI **COMPLEMENT** RECEPTOR IS AN INHIBITOR OF THE **COMPLEMENT** CASCADE.
AU IIDA K; NUSSENZWEIG V
CS DEP. PATHOL., N.Y. MED. CENT., NEW YORK, 10016, USA.
SO J EXP MED 153 (5). 1981. 1138-1150. CODEN: JEMEAV ISSN: 0022-1007
LA English
AB A glycoprotein from the membrane of human erythrocytes was identified as a receptor for C3b (b fragment of **complement** component 3) (CR1). It promotes the dissociation of the alternative pathway C3 convertase C3b,Bb and the cleavage of C3b by C3b/C4b inactivator. CR1

also inactivates the C3 and **C5** convertases of the classical pathway. CR1 inhibits the consumption of C3 by C3 convertase EAC142 (sheep erythrocyte-**antibody-complement** complex) and enhances the decay of C4b,2a sites. On a weight basis, CR1 is 5-10 times more active than C4 binding protein, a serum inhibitor of C4b,2a. The binding of 125I-CR1 to EAC14 cells is inhibited by C2. CR1 and C2 probably compete for a site on C4b. CR1 inhibited **C5** convertase even more effectively, but had no effect on the assembly of the late **complement** components. At high concentrations, CR1 alone has no irreversible effects on cell-bound C4b. In the fluid phase, CR1 can function as a cofactor for the cleavage of the .**alpha**.' **chain** of C4b by C3b/C4b inactivator. A well-known function of CR1 is to promote adherence of microbes or immune complexes bearing C3b and C4b to cells. This interaction could result in a microenvironment damaging to the plasma membrane of the responding cell because the extrinsic C3b and C4b fragments can serve as additional sites of assembly of enzymes of the cascade. CR1 on the surface of cells may supply an increased local concentration of a strong inhibitor of the amplifying enzymes of the **complement** system and may provide cells with a mechanism for circumventing damage when they bind C3b- and C4b-bearing substrates.

L12 ANSWER 13 OF 13 BIOSIS COPYRIGHT 1997 BIOSIS
AN 80:162533 BIOSIS
DN BA69:37529
TI BIOSYNTHESIS OF A SINGLE CHAIN PRO **COMPLEMENT** C-5 BY NORMAL MOUSE LIVER MESSENGER RNA ANALYSIS OF THE MOLECULAR BASIS OF **COMPLEMENT** C-5 DEFICIENCY IN AKR-J MICE.
AU PATEL F; MINTA J O
CS DEP. PATHOL., UNIV. TORONTO, TORONTO, ONT. M5S 1A8, CAN.
SO J IMMUNOL 123 (5). 1979. 2408-2414. CODEN: JOIMA3 ISSN: 0022-1767
LA English
AB An in vivo labeling technique was used to prove the molecular lesions precipitating in **C5** [**complement** component 5] deficiency in the AKR/J mouse. 14C-labeled amino acids were administered i.p. into normal and **C5**-deficient mice and the plasma was harvested 4 h later. By using monospecific **anti-C5**, newly synthesized 14C-**C5** was immunoprecipitated from the plasma and postmitochondrial supernatants (PMS) of a liver homogenate. SDS-PAGE [sodium dodecyl sulfate-polyacrylamide gel electrophoresis] analysis demonstrated that normal mouse plasma (apparent MW 205,000) was composed of 2 dissimilar subunits, an .**alpha**.-**chain** (115,000 daltons) and a .beta.-chain (82,000). Nonsecreted **C5** immunoprecipitated from the PMS was resolved into 2 nonreducible polypeptide chains of MW 200,000 and 170,000 respectively. By comparison to plasma **C5**, the 170,000 dalton peak polypeptide chain probably represents incompletely synthesized, partially degraded or unglycosylated pro-**C5**. 14C-**C5** immunoprecipitates from the plasma and the PMS of AKR/J **C5**-deficient mice contained insignificant radioactivity and on SDS gels did not resolve into any distinct peaks, suggesting that **C5** is not synthesized in this strain. 14C-C3 immunoprecipitated from the plasma of normal and AKR/J mice in each case was composed of covalently-linked .**alpha**.- and .beta.-**chains** (MW 130,000 and 85,000, respectively). 14C-C3 immunoprecipitated from the PMS of normal and **C5**-deficient liver homogenates in each case migrated on SDS gels as a single polypeptide chain, pro-C3 (MW 200,000). These findings were confirmed by cell-free translation studies. Poly(A)-mRNA isolated

from normal mouse liver stimulated the incorporation of 3H-leucine into protein in a time-dependent fashion in a reticulocyte lysate system [rabbit] under optimal conditions. 3H-**C5** immunoprecipitated from the translation reaction mixture behaved as a single nonreducible polypeptide chain (MW 170,000). Poly A-mRNA from the liver of the AKR/J mouse displayed similar kinetics and dose-response stimulation of protein synthesis upon translation in the cell-free system, but failed to direct the synthesis of **C5** or **C5** immunoreactive peptides, although C3 was synthesized normally as pro-C3. Since the intact machinery for carbohydrate synthesis is not present in the reticulocyte cell-free system, the 170,000-dalton **C5** polypeptide chain is possibly unglycosylated pro-**C5**. Thus, **C5** is synthesized as a single-chain pro-**C5** and post-translationally converted to a two-subunit **C5** molecule by limited proteolysis. In the AKR/J **C5**-deficient mouse **C5** is not synthesized at all, suggesting the lack of a functional mRNA for **C5** in this strain.

L14 ANSWER 1 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 97:296290 BIOSIS
DN 99595493
TI Inhibition of **complement** activity by humanized anti-**C5** antibody and single-chain Fv.
AU Thomas T C; **Rollins S A**; Rother R P; Giannoni M A; Hartman S L; Elliott E A; **Nye S H**; **Matis L A**; Squinto S P; **Evans M J**
CS Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511, USA
SO Molecular Immunology 33 (17-18). 1996 (1997). 1389-1401. ISSN: 0161-5890
LA English
AB Activation of the **complement** system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal antibody (5G1.1) that recognizes the human **complement** protein **C5**, has been shown to effectively block **C5** cleavage, thereby preventing the generation of the pro-inflammatory **complement** components C5a and C5b-9. Humanized 5G1.1 antibody, Fab and scFv molecules have been produced by grafting the complementarity determining regions of 5G1.1 on to human framework regions. Competitive ELISA analysis indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to **C5**, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv molecules blocked **complement**-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete **complement** inhibition occurring at a three-fold molar excess, relative to the human **C5** concentration. In contrast to a previously characterized anti-**C5** scFv molecule, the humanized h5G1.1 scFv also effectively blocked C5a generation. Finally, an intact humanized h5G1.1 antibody blocked human **complement** lytic activity at concentrations identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivatives retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these molecules may serve as potent inhibitors of **complement**-mediated pathology in human

inflammatory diseases.

L14 ANSWER 2 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 97:147682 BIOSIS
DN 99446885
TI Monoclonal antibody to **C5** inhibits C5a and C5b-9 generation without inhibition of C3 cleavage and significantly limits myocardial ischemia and reperfusion induced tissue damage.
AU Vakeva A; **Rollins S A; Matis L A;** Stahl G L
CS Brigham Women's Hosp., Boston, MA, USA
SO 46th Annual Scientific Session of the American College of Cardiology, Anaheim, California, USA, March 16-19, 1997. Journal of the American College of Cardiology 29 (2 SUPPL. A). 1997. 267A. ISSN: 0735-1097
DT Conference
LA English

L14 ANSWER 3 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 96:501911 BIOSIS
DN 99224267
TI Subcutaneous administration of anti-**C5** monoclonal antibody induces systemic **complement** inhibition and ameliorates immune complex mediated inflammatory responses.
AU Wang Yi; Hu Q; Kristan J; **Rollins S; Evans M;** Madri J; **Matis L**
CS Alexion Pharm. Inc., 25 Science Park, New Haven, CT 06511, USA
SO 60th National Scientific Meeting of the American College of Rheumatology and the 31st National Scientific Meeting of the Association of Rheumatology Health Professionals, Orlando, Florida, USA, October 18-22, 1996. Arthritis & Rheumatism 39 (9 SUPPL.). 1996. S245. ISSN: 0004-3591
DT Conference
LA English

L14 ANSWER 4 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 96:413396 BIOSIS
DN 99135752
TI Amelioration of lupus-like autoimmune disease in NZB-W F-1 mice after treatment with a blocking monoclonal antibody specific for **complement** component **C5**.
AU Wang Yi; Hu Q; Madri J A; **Rollins S A;** Chodera A; **Matis L A**
CS Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511, USA
SO Proceedings of the National Academy of Sciences of the United States of America 93 (16). 1996. 8563-8568. ISSN: 0027-8424
LA English
AB New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic **complement** activation, the role of proinflammatory **complement** components in disease progression has not been established. In this study we have examined the contribution of activated terminal **complement** proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal antibody (mAb) specific for the **C5** component of **complement** that blocks

the cleavage of **C5** and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-**C5** mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal **complement** cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated **C5** inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

L14 ANSWER 5 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 96:107988 BIOSIS
DN 98680123
TI In vitro and in vivo inhibition of **complement** activity by a single-chain Fv fragment recognizing human **C5**.
AU **Evans M J**; **Rollins S A**; Wolff D W; Rother R P; Norin A J; Therrien D M; Grijalva G A; Mueller J P; **Nye S H** ; Squinto S P; Wilkins J A
CS Dep. Molecular Dev., Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511, USA
SO Molecular Immunology 32 (16). 1995. 1183-1195. ISSN: 0161-5890
LA English
AB **Complement** activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal antibody (N19-8) that recognizes the human **complement** protein **C5** has been shown to effectively block the cleavage of **C5** into C5a and C5b, thereby blocking terminal **complement** activation. In this study, a recombinant N19-8 scFv antibody fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human **C5** and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit **complement**-mediated tissue damage, **complement** -dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer containing 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approximately 10 min after the addition of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 hr following the addition of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma containing the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 hr. Pharmacokinetic analysis of N19-8 scFv serum levels suggested a two-compartment model with a T-1/2-alpha of 27 min. Together, these data suggest the recombinant N19-8 scFv is a potent inhibitor of the terminal **complement** cascade and may have potential in vivo applications where short duration inhibition of terminal **complement** activity is desirable.

L14 ANSWER 6 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:61239 BIOSIS
DN 98633374
TI Monoclonal antibodies directed against human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs.
AU **Rollins S A**; **Matis L A**; Springhorn J P; Setter E; Wolff D W
CS Dep. Immunol., Alexion Pharmaceutical Inc., 25 Science Park, New Haven, CT 06511, USA
SO Transplantation (Baltimore) 60 (11). 1995. 1284-1292. ISSN: 0041-1337
LA English
AB The hyperacute rejection (HAR) of xenotransplanted organs is initiated by the deposition of natural antibodies on donor endothelium followed by the activation of the recipient **complement** system, which rapidly destroys the graft. Studies of the role of activated **complement** in HAR have suggested that natural antibody as well as early (C3a, C3b) and late (C5a, C5b-9) activated **complement** components may contribute to cell activation and damage. Attenuation of HAR has been achieved by blockade of C3 activation with soluble CR1 or consumptive depletion of **complement** with cobra venom factor; however, similar studies using specific inhibitors of terminal **complement** components have not been described. To address the contribution of C5a and the membrane attack complex (C5b-9, MAC) to **complement**-mediated xenogeneic cell and organ damage, we utilized functionally blocking monoclonal antibodies directed against the human terminal **complement** components **C5** and C8. Our data show that both anti-**C5** and anti-C8 mAbs protect porcine aortic endothelial cells from membrane damage mediated by human C5b-9. Additionally, both the anti-**C5** and anti-C8 mABs blocked **complement**-mediated generation of membrane prothrombinase activity on porcine aortic endothelial cells challenged with human serum. To test the ability of these antibodies to attenuate antibody and **complement**-mediated damage of xenogeneic organs, an ex vivo model was developed wherein isolated rat hearts were perfused with human serum in the presence or absence of the anti-**C5** and anti-C8 mAbs. Our data demonstrate that mAbs directed against human **C5** and C8 prevented organ damage by human serum **complement** and suggest that these molecules may serve as potent inhibitors of HAR.

L14 ANSWER 7 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 96:61228 BIOSIS
DN 98633363
TI **Complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation.
AU Kroshus T J; **Rollins S A**; Dalmasso A P; Elliott E A; **Matis L A**; Squinto S P; Bolman R M III
CS Dep. Surgery, Univ. Minn., Box 207, UMHC, 420 Delaware St. SE, Minneapolis, MN 55455, USA
SO Transplantation (Baltimore) 60 (11). 1995. 1194-1202. ISSN: 0041-1337
LA English
AB Prevention of hyperacute xenograft rejection in the pig-to-primate combination has been accomplished by removal of natural antibodies, **complement** depletion with cobra venom factor, or prevention of C3 activation with the soluble **complement** inhibitor

sCR1. Although these strategies effectively prevent hyperacute rejection, they do not address the relative contribution of early (C3a, C3b) versus late (C5a, C5b-9) activated **complement** components to xenogeneic organ damage. To better understand the role of the terminal **complement** components (C5a, C5b-9) in hyperacute rejection, an anti-human **C5** mAb was developed and tested in an ex vivo model of cardiac xenograft rejection. In vitro studies demonstrated that the anti-**C5** mAb effectively blocked **C5** cleavage in a dose-dependent manner that resulted in complete inhibition of both C5a and C5b-9 generation. Addition of anti-**C5** mAb to human blood used to perfuse a porcine heart prolonged normal sinus cardiac rhythm from a mean time of 25.2 min in hearts perfused with unmodified blood to 79,296, or gt 360 min when anti-**C5** mAb was added to the blood at 50 mu-g/ml, 100 mu-g/ml, or 200 mu-g/ml, respectively. In these experiments, activation of the classical **complement** pathway was completely inhibited. Hearts perfused with blood containing the highest concentration of anti-**C5** mAb had no histologic evidence of hyperacute rejection and no deposition of C5b-9. These experiments suggest that the activated terminal **complement** components C5a and C5b-9, but not C3a or C3b, play a major role in tissue damage in this porcine-to-human model of hyperacute rejection. They also suggest that targeted inhibition of terminal **complement** activation by anti-**C5** mAbs may be useful in clinical xenotransplantation.

L14 ANSWER 8 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:549139 BIOSIS
DN 98563439
TI A novel bifunctional chimeric **complement** inhibitor that regulates C3 convertase and formation of the membrane attack complex.
AU Fodor W L; **Rollins S A**; Guilmette E R; Setter E; Squinto S P
CS Alexion Pharmaceuticals Inc., 25 Science Park, Suite 360, New Haven, CT 06511, USA
SO Journal of Immunology 155 (9). 1995. 4135-4138. ISSN: 0022-1767
LA English
AB Human cells express cell surface **complement** regulatory molecules that inhibit the activity of the C3/**C5** convertases (DAF, MCP, CR1) or inhibit the membrane attack complex (CD59). A single molecule that inhibits both the convertase activity and formation of the membrane attack complex has never been characterized. To this end, we have developed two reciprocal chimeric **complement** inhibitors (CD, NH2-CD59-DAF-GPI; and DC, NH2-DAF-CD59-GPI) that contain the functional domains of decay accelerating factor (DAF; CD55) and CD59. Cell surface expression of the CD and DC chimeric proteins was detected with DAF- and CD59-specific antisera. Cell surface C3d deposition was inhibited on cells expressing the chimeric molecules, thereby indicating that the DAF moiety was functional in both molecules. Conversely, Ab-blocking experiments demonstrated that only the DC molecule retained CD59 function. Therefore, the DC molecule represents a novel potent chimeric bifunctional **complement** inhibitor that retains the functional domains of two distinct **complement** regulatory molecules.

L14 ANSWER 9 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:521823 BIOSIS
DN 98536123

TI Anti-**C5** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.
AU Wang Y; **Rollins S**; Madri J; **Matis L**
CS Alexion Pharmaceutical Inc., 25 Science Park, New Haven, CT 06511, USA
SO 59th National Scientific Meeting of the American College of Rheumatology and the 30th National Scientific Meeting of the Association of Rheumatology Health Professionals, San Francisco, California, USA, October 21-26, 1995. Arthritis & Rheumatism 38 (9 SUPPL.). 1995. S372. ISSN: 0004-3591
DT Conference
LA English

L14 ANSWER 10 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:511655 BIOSIS
DN 98516705
TI Anti-**C5** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.
AU Wang Y; **Rollins S A**; Madri J A; **Matis L A**
CS Immunobiol. Program, Alexion Pharm. Inc., New Haven, CT 06511, USA
SO Proceedings of the National Academy of Sciences of the United States of America 92 (19). 1995. 8955-8959. ISSN: 0027-8424
LA English
AB Activated components of the **complement** system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target **complement** activation in immune-mediated joint inflammation, we have utilized monoclonal antibodies (mAbs) that inhibit the **complement** cascade at **C5**, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, we demonstrate the efficacy of a mAb specific for murine **C5** in the treatment of collagen-induced arthritis, an animal model for RA. We show that systemic administration of the anti-**C5** mAb effectively inhibits terminal **complement** activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-**C5** mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a critical role for activated terminal **complement** components not only in the induction but also in the progression of collagen-induced arthritis and suggest that **C5** may be an attractive therapeutic target in RA.

L14 ANSWER 11 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:479674 BIOSIS
DN 98493974
TI Blockade of C5a and C5b-9 generation inhibits leukocyte and platelet activation during extracorporeal circulation.
AU Rinder C S; Rinder H M; Smith B R; Fitch J C K; Smith M J; Tracey J B; **Matis L A**; Squinto S P; **Rollins S A**
CS Dep. Anesthesiol., Tompkins 3, Yale Univ. Sch. Med., 333 Cedar St., New Haven, CT 06510, USA
SO Journal of Clinical Investigation 96 (3). 1995. 1564-1572. ISSN: 0021-9738
LA English
AB **Complement** activation contributes to the systemic inflammatory response induced by cardiopulmonary bypass. At the cellular level, cardiopulmonary bypass activates leukocytes and

platelets; however the contribution of early (C3a) versus late (C5a, soluble C5b-9) **complement** components to this activation is unclear. We used a model of simulated extracorporeal circulation that activates **complement** (C3a, C5a, and C5b-9 formation), platelets (increased percentages of P-selectin-positive platelets and leukocyte-platelet conjugates), and neutrophils (upregulated CD11b expression). To specifically target **complement** activation in this model, we added a blocking mAb directed at the human **C5 complement** component and assessed its effect on **complement** and cellular activation. Compared with a control mAb, the anti-human **C5** mAb profoundly inhibited C5a and soluble C5b-9 generation and serum **complement** hemolytic activity but had no effect on C3a generation. Additionally, the anti-human **C5** mAb significantly inhibited neutrophil CD11b upregulation and abolished the increase in P-selectin-positive platelets and leukocyte-platelet conjugate formation compared to experiments performed with the control mAb. This suggests that the terminal components C5a and C5b-9, but not C3a, directly contribute to platelet and neutrophil activation during extracorporeal circulation. Furthermore, these data identify the **C5** component as a site for therapeutic intervention in cardiopulmonary bypass.

L14 ANSWER 12 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:458966 BIOSIS
DN 98473266
TI **Complement**-specific antibodies: Designing novel antiinflammatories.
AU **Matis L A; Rollins S A**
CS Immunobiol. Program, Alexion Pharm. Inc., 25 Science Park, Suite 360, New Haven, CT 06511, USA
SO Nature Medicine 1 (8). 1995. 839-842. ISSN: 1078-8956
LA English

L14 ANSWER 13 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:409606 BIOSIS
DN 98423906
TI Rapid expression of an anti-human **C5** chimeric Fab utilizing a vector that replicates in COS and 293 cells.
AU **Evans M J**; Hartman S L; Wolff D W; **Rollins S A**; Squinto S P
CS Dep. Mol. Dev., Alexion Pharm. Inc., 25 Science Park, New Haven, CT 06511, USA
SO Journal of Immunological Methods 184 (1). 1995. 123-138. ISSN: 0022-1759
LA English
AB Inhibition of **complement** system activation requires the development of soluble nonimmunogenic inhibitors with good tissue penetrating abilities that are themselves unable to activate **complement**, Chimeric mouse/human Fabs capable of blocking the activity of **complement** proteins are likely to fulfill these criteria. Several monoclonal antibodies that inhibit the activation of the human **complement** system have recently been developed. To examine the properties of chimeric Fab derived from these monoclonal antibodies, we have developed an expression system which allows the rapid production of milligram quantities of chimeric Fab. Both the chimeric light chain and the chimeric Fd were co-expressed from the same vector, pAPEX-3P. This vector contains the SV40 origin of replication, which allows the rapid production of

chimeric Fab in COS cells for preliminary characterization. Additionally, pAPEX-3P contains the Epstein-Barr virus origin of replication and a puromycin selectable marker for maintenance as a stable episome in human cell lines. A production system consisting of transfected 293-EBNA cells cultured in serum free medium followed by protein G-Sepharose chromatography of the conditioned medium was found to be sufficient for the rapid production of purified chimeric Fab. Here we have utilized this expression system to demonstrate that an anti-human **C5** chimeric Fab was a potent inhibitor of **complement** activation in both in vitro activation assays and an ex vivo model of **complement**-mediated tissue damage.

L14 ANSWER 14 OF 14 BIOSIS COPYRIGHT 1997 BIOSIS
AN 95:288324 BIOSIS
DN 98302624
TI Monoclonal antibodies to **complement** component **C5** in the therapy of inflammatory joint disease.
AU Wang Y; **Rollins S R**; Madri J A; Elliott E A; **Matis L A**
CS Alexion Pharm., New Haven, CT, USA
SO Clinical Research Meeting, San Diego, California, USA, May 5-8, 1995. Journal of Investigative Medicine 43 (SUPPL. 2). 1995. 362A.
DT Conference
LA English

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L2   (        51)SEA FILE=HCAPLUS ABB=ON  "EVANS MARK"/AU OR ("EVANS MARK
                 J"/AU OR "EVANS MARK JAMES"/AU)
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                 R "NYE STEVEN H"/AU OR "NYE STEVEN HOWARD"/AU)
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                 R"/AU) OR ("ROLLINS SCOTT"/AU OR "ROLLINS SCOTT A"/AU OR
                 "ROLLINS SCOTT ALAN"/AU)
L9           795 SEA FILE=HCAPLUS ABB=ON  L8 OR L7



     (FILE 'HCAPLUS' ENTERED AT 10:20:41 ON 29 JUL 1997)
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L10          469 S COMPLEMENT AND  C5
L11           12 S L10 AND L9
L12         5933 S ALPHA (2W) CHAIN# OR (ALPAH (2W) CHAIN#)/AB
L13        13740 S L12 OR (ALPHA (2W) CHAIN#)/AB
L14           33 S L13 AND L10
L15            3 S L14 AND (ANTI OR ANTIBOD?)
L16           12 S L11 NOT L15

     FILE 'HCAPLUS' ENTERED AT 10:22:53 ON 29 JUL 1997

=> d .ca l15 1-3;d .ca 1-12

L15  ANSWER 1 OF 3  HCAPLUS  COPYRIGHT 1997 ACS
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AN 1993:122866 HCAPLUS
DN 118:122866
TI Molecular basis of **complement** resistance of human melanoma cells expressing the C3-cleaving membrane protease p65
AU Ollert, Markus W.; Kadlec, Joseph V.; Petrella, Eugene C.; Bredehorst, Reinhard; Vogel, Carl Wilhelm
CS Sch. Med., Georgetown Univ., Washington, DC, 20007, USA
SO Cancer Res. (1993), 53(3), 592-9
CODEN: CNREA8; ISSN: 0008-5472
DT Journal
LA English
AB The mol. mechanism of complement resistance of the human SK-MEL-170 melanoma cell line was investigated. The cells have been shown to express the C3b-cleaving membrane protease p65. To delineate the mol. consequences of the C3b-cleaving activity for the complement cytotoxicity, the mol. events during the initiation (R24 monoclonal antibody, C1), amplification (C4, C3), and membrane attack (C5, C9) phases of complement were studied in comparison to a complement-susceptible human melanoma line (SK-MEL-93-2). No cleavage of C4b and C5b, 2 mols. structurally similar to C3b, was obsd. on the cells during classical pathway activation indicating the specificity of the p65 protease for the C3b mol. The rapid degrdn. of C3b by p65 on the surface of complement-resistant SK-MEL-170 cells generates a mol. wt. 30,000 C3.**alpha**.'-**chain**-fragment detectable as early as 1 min after complement activation, whereas no such fragment was present in detectable amts. on complement-susceptible cells. As a result of the rapid C3b proteolysis by p65 on resistant SK-MEL-170 cells, less C5 convertases are formed, which in turn results in the formation of a lower no. of terminal complement components and membrane attack complexes. R24 antibody and C1q binding to the resistant cells was slightly lower as to susceptible cells. C4 binding studies, however, revealed that the obsd. difference in antibody and C1q binding has no influence on the complement resistance of SK-MEL-170 cells: more C4b was bound to complement-resistant (1565 fg/cell) as compared to susceptible cells (715 fg/cell). On extn. of the mol. forms of C4 bound to the cell membranes, an addnl. high mol. wt. C4 species, apparently a C4b-C4b homodimer, appeared only on the resistant SK-MEL-170 cells that may function as a residual back-up C5 convertase. Thus, collectively, SK-MEL-170 human melanoma cells evade complement-mediated cytolysis despite sufficient activation of early components of the classical complement pathway by p65-mediated rapid degrdn. of surface-bound C3b, leading to a redn. in membrane attack complex formation. Rapid cleavage of surface deposited C3b was thus established as a powerful mechanism of complement resistance.
CC 15-8 (Immunochemistry)
ST **complement** resistance melanoma C3b protease p65
IT Melanoma
(**complement** resistance by human, C3b-cleaving membrane protease p65 in)
IT Cytolysis
(**complement**-mediated, human melanoma cell resistance to, membrane protease in)
IT Cell membrane
(protease p65 of, of human melanoma cells, in resistance to **complement**)
IT **Complement**
RL: BIOL (Biological study)

(classical pathway, melanoma cells resistance to, of humans, membrane protease in)

IT **Antibodies**
RL: BIOL (Biological study)
(monoclonal, to ganglioside GD3 on human melanoma cells, **complement** activation by, melanoma resistance to, membrane protease in)

IT 62010-37-1, Ganglioside GD3
RL: BIOL (Biological study)
(**antibody** to, **complement** activation by, human melanoma cells resistance to, C3b-cleaving membrane protease in)

IT 60831-94-9, **Complement C5** convertase
82986-89-8, **Complement** C 5b9
RL: FORM (Formation, nonpreparative)
(formation of, human melanoma cell inhibition of, C3b-cleaving membrane protease in)

IT 80295-50-7, **Complement** C4b
RL: BIOL (Biological study)
(homodimer of, on human melanoma cells, membrane protease and **complement** resistance in relation to)

IT 80295-41-6, **Complement** C3
RL: BIOL (Biological study)
(melanoma cell binding of human, membrane protease and **complement** resistance in relation to)

IT 80295-43-8, **Complement** C3b
RL: BIOL (Biological study)
(membrane protease p65 of human melanoma cell hydrolysis of, **complement** resistance in relation to)

IT 128689-72-5, **Complement** C3b proteinase
RL: BIOL (Biological study)
(of melanoma cells of humans, in **complement** resistance)

L15 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1988:547624 HCAPLUS
DN 109:147624
TI Use of antisera to the isolated alpha and beta subunits of C3 as probes to study functional sites present on particle-bound C3b but absent on native soluble forms of C3
AU Whaley, K.; Nilsson, Ulf
CS West. Infirm., Univ. Glasgow, Glasgow, UK
SO Int. Arch. Allergy Appl. Immunol. (1988), 86(1), 55-61
CODEN: IAAAAM; ISSN: 0020-5915
DT Journal
LA English
AB The effect of antisera to the isolated .**alpha**. and .beta. **chains** of complement C3 on certain C3b-dependent reactions has been studied. C5-mediated hemolysis of erythrocyte-antibody-C1423b was inhibited preferentially by antiserum to the .**alpha**. **chain**, whereas antiserum to the .beta. chain inhibited the formation of C3bBb. The anti-.beta. chain antiserum also stabilized C3bBbP, and rendered the enzyme relatively resistant to accelerated decay in the presence of factor H. These and previous findings that anti-.alpha. and anti-.beta. IgG bind to restricted subsets of antigenic determinants on C3/C3b suggest that these antisera affect C3b function through the binding of antibodies to active binding sites exclusively exposed by bound C3b.
CC 15-4 (Immunochemistry)
ST **complement** C3 alpha beta subunit **antibody**
IT Hemolysis

(**complement** C3-mediated, **antibodies** to C3 subunits effect on, of humans)
IT **Antibodies**
RL: BIOL (Biological study)
(to **complement** C3 subunits, **complement** C3-mediated activities response to, of humans)
IT 80295-43-8, **Complement** C3b
RL: BIOL (Biological study)
(**antibodies** to C3 subunits effect on activities of, of humans)
IT 80295-65-4
RL: BIOL (Biological study)
(**complement** convertase resistance to, **antibodies** to **complement** C3 subunits effect on, of humans)
IT 80295-53-0, **Complement C5**
RL: BIOL (Biological study)
(hemolysis mediated by, **antibodies** to **complement** C3 subunits effect on, of humans)
IT 77000-02-3
RL: PROC (Process)
(stabilization of, by **antibodies** to C3 subunits, of humans)
IT 80295-41-6, **Complement** C3
RL: BIOL (Biological study)
(.alpha.- and .beta.-subunits of, **antibodies** to, C3-mediated activities response to, of humans)

L15 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 1997 ACS
AN 1986:146822 HCAPLUS
DN 104:146822
TI Parameters of the stimulation of human monocytes by factor B of the **complement** system
AU Baumgarten, H.; Opperman, M.; Schulze, M.; Goetze, O.
CS Zent. Hyg. Humangenet., Universitaetsklin. Goettingen, Goettingen, D-3400, Fed. Rep. Ger.
SO Mononucl. Phagocytes, [Proc. Conf.], 4th (1985), Meeting Date 1984, 163-71. Editor(s): Van Furth, Ralph. Publisher: Nijhoff, Dordrecht, Neth.
CODEN: 54WAAX
DT Conference
LA English
AB Evidence is provided for a complement factor B (Bb)-dependent stimulation of human monocytes with respect to the secretion of lysosomal hydrolases and H2O2 and to receptor-mediated phagocytosis. It is further demonstrated that divalent antibody mols. specific for the C5a region of the .**alpha**.-**chain** of C5 are able to induce the secretion of lysosomal hydrolases in the absence of any other added stimulus. Probably membrane-assocd. (m)C5 is oriented in the monocyte plasma membrane in such a way that the C5a portion of its .**alpha**.-**chain** is accessible to antibody added to the outside of the cell. Apparently, the cleavage site for Bb on the .**alpha**.-**chain** of mC5 is externally disposed, so the obsd. effects of Bb on human monocytes are caused by the generation of mC5 and C5a.
CC 15-4 (Immunochemistry)
ST monocyte stimulation **complement** factor Bb
IT Phagocytosis
(by macrophage, **complement** factor Bb stimulation of, of

human)
IT Monocyte
(hydrogen peroxide and hydrolase release from and phagocytosis by, **complement** factor Bb stimulation of, of human)
IT Lysosome
(hydrolases of, **complement** factor Bb-stimulated release of, from human macrophage)
IT **Antibodies**
RL: BIOL (Biological study)
(to **complement** C5a, lysosomal hydrolase release from human monocyte induction by, **complement** factor Bb in relation to)
IT 80295-54-1
RL: FORM (Formation, nonpreparative)
(formation of, factor Bb stimulation of human monocyte response to, membrane-assocd. **C5** in relation to)
IT 82532-87-4
RL: BIOL (Biological study)
(hydrogen peroxide and hydrolase release and phagocytosis by macrophage induction by, **complement C5** in relation to, of human)
IT 7722-84-1, biological studies 9001-77-8 9012-33-3
RL: BIOL (Biological study)
(release of, from monocyte of human, **complement** factor Bb stimulation of)

L16 ANSWER 1 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1997:430905 HCAPLUS
TI Amelioration of lupuslike autoimmune disease in NZB/W F1 mice after treatment with a blocking monoclonal antibody specific for **complement** component **C5**
AU Wang, Yi; Hu, Qile; Madri, Joseph A.; **Rollins, Scott A.**; Chodera, Amy; **Matis, Louis A.**
CS Alexion Pharmaceuticals, 25 Science Park, New Haven, CT, 06511, USA
SO Controlling Complement Syst. Novel Drug Dev., [IBC Conf.] (1997), 89-109. Editor(s): Mazarakis, Helen; Swart, Sarah Jane. Publisher: International Business Communications, Southborough, Mass. CODEN: 64QOAM
DT Conference
LA English
AB New Zealand black .times. New Zealand white (NZB/W) F1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus (SLE). Female NZB/W F1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 mo of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of pro-inflammatory complement components in disease progression has not been established. In this study we have examd. the contribution of activated terminal complement proteins to the pathogenesis of the lupuslike autoimmune disease. Female NZB/W F1 mice were treated with a monoclonal antibody (mAb) specific for the C5 component of complement that blocks the coverage of C5 and thus prevents the generation of the potent pro-inflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for six months resulted in significant amelioration of the course of
CC 15 (Immunochemistry)

L16 ANSWER 2 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1997:348505 HCAPLUS
TI Inhibition of **complement** activity by humanized anti-**C5** antibody and single-chain Fv
AU Thomas, Thomas C.; **Rollins, Scott A.**; Rother, Russell P.; Giannoni, Michelle A.; Hartman, Sandra L.; Elliott, Eileen A.; **Nye, Steven H.**; **Matis, Louis A.**; Squinto, Stephen P.; **Evans, Mark J.**
CS Alexion Pharmaceuticals, New Haven, CT, 06511, USA
SO Mol. Immunol. (1997), 33(17/18), 1389-1401
CODEN: MOIMD5; ISSN: 0161-5890
PB Elsevier
DT Journal
LA English
AB Activation of the complement system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal antibody (5G1.1) that recognizes the human complement protein C5, has been shown to effectively block C5 cleavage, thereby preventing the generation of the pro-inflammatory complement components C5a and C5b-9. Humanized 5G1.1 antibody, Fab and scFv mols. have been produced by grafting the complementarity detg. regions of 5G1.1 on to human framework regions. Competitive ELISA anal. indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to C5, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv mols. blocked complement-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete complement inhibition occurring at a three-fold molar excess, relative to the human c5 concn. In contrast to a previously characterized anti-C5 scFv mol., the humanized h5G1.1 scFv also effectively blocked C5a generation. Finally, an intact humanized h5G1.1 antibody blocked human complement lytic activity at concns. identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivs. retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these mols. may serve as potent inhibitors of complement-mediated pathol. in human inflammatory diseases.
CC 15 (Immunochemistry)

L16 ANSWER 3 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:498766 HCAPLUS
DN 125:165528
TI Amelioration of lupus-like autoimmune disease in NZB/W F1 mice after treatment with a blocking monoclonal antibody specific for **complement** component **C5**
AU Wang, Yi; Hu, Qile; Madri, Joseph A.; **Rollins, Scott A.**; Chodera, Amy; **Matis, Louis A.**
CS Immumobiology Program, Alexion Pharmaceuticals, Inc., New Haven, CT, 06511, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1996), 93(16), 8563-8568
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB New Zealand black .times. New Zealand white (NZB/W) F1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F1

mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 mo of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. Here, the authors examd. the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F1 mice were treated with a monoclonal antibody (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 mo resulted in amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB/W F1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

CC 15-8 (Immunochemistry)
ST lupus model monoclonal antibody **complement C5**
IT Lupus erythematosus
(terminal **complement** cascade role in lupus erythematosus model)
IT Kidney, disease
(immune complex glomerulonephritis, terminal **complement** cascade role in lupus erythematosus model)
IT Antibodies
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, amelioration of lupus-like autoimmune disease in mice after treatment with blocking monoclonal antibody to **complement** component **C5**)
IT 80295-53-0, **Complement C5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(amelioration of lupus-like autoimmune disease in mice after treatment with blocking monoclonal antibody to **complement** component **C5**)
IT 82986-89-8, **Complement** C5b-9
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(terminal **complement** cascade role in lupus erythematosus model)

L16 ANSWER 4 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:365806 HCAPLUS
DN 125:26270
TI Methods for the treatment of inflammatory joint disease with compounds that block **complement** component **C5**
IN Wang, Yi; **Matis, Louis**
PA Alexion Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
PI WO 9609043 A1 960328
DS W: AU, CA, JP
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AI WO 95-US12404 950921
PRAI US 94-311489 940923
DT Patent
LA English

AB The use of compds. that block complement component C5 or its active fragments C5a and/or C5b (collectively referred to as "C5 blockers") to treat established joint inflammation (arthritis) is disclosed. Administration of such C5 blockers has been found to (1) arrest and/or reduce inflammation in joints which are already inflamed and (2) inhibit the spread of inflammation to unaffected joints. The C5 blockers include e.g. proteins (including antibodies) and peptides. Results using a monoclonal antibody C5 blocker are presented.

IC ICM A61K031-395
ICS A61K031-34; C07D307-94; C07K016-18; C07K016-40

CC 1-7 (Pharmacology)
Section cross-reference(s): 15

ST **complement C5** blocker antiinflammatory arthritis; monoclonal antibody **complement C5** antiarthritic

IT Cytolysis
(by **complement; complement C5** blockers for treatment of inflammatory joint disease)

IT Inflammation inhibitors
(**complement C5** blockers for treatment of inflammatory joint disease)

IT Blood serum
Blood
(**complement C5** blockers for treatment of inflammatory joint disease in relation to redn. of cell-lysing ability of **complement** in blood-derived fluid)

IT Synovial fluid
(**complement C5** blockers for treatment of inflammatory joint disease in relation to redn. of cell-lysing ability of **complement** in synovial fluid)

IT **Complement**
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(cytolysis by; **complement C5** blockers for treatment of inflammatory joint disease)

IT Inflammation inhibitors
(antiarthritics, **complement C5** blockers for treatment of inflammatory joint disease)

IT Joint, anatomical
(disease, inflammation, **complement C5** blockers for treatment of inflammatory joint disease)

IT Antibodies
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, anti-**C5; complement C5** blockers for treatment of inflammatory joint disease)

IT 80295-53-0, **Complement C5** 80295-54-1, **Complement** C5a 80295-55-2, **Complement** C5b 82986-89-8, **Complement** C5b9
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(**complement C5** blockers for treatment of inflammatory joint disease)

L16 ANSWER 5 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:298330 HCAPLUS
DN 124:325364
TI Retroviral transduction of cells using soluble **complement** inhibitors

IN Rother, Russell P.; **Rollins, Scott A.**; Mason, James M.; Squinto, Stephen P.
PA Alexion Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 49 pp.
CODEN: PIXXD2
PI WO 9603146 A1 960208
DS W: AU, CA, JP
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AI WO 95-US8924 950714
PRAI US 94-278550 940721
DT Patent
LA English
AB Methods and compns. are provided for facilitating gene therapy procedures involving the transduction of target cells with retroviral vector particles in the presence of complement-contg. body fluids. The administration of sol. complement inhibitor mols. to body fluids prevents the complement-mediated inactivation of the retroviral vector particles, and provides a safety mechanism for such gene therapy procedures, as the action of sol. complement inhibitors is transient, and any retroviral vector particles present after the return of uninhibited complement activity will be inactivated.
IC ICM A61K039-395
CC 63-3 (Pharmaceuticals)
Section cross-reference(s): 1
ST retrovirus transduction **complement** inhibitor gene therapy
IT **Complement**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitors; retroviral transduction of cells using sol. **complement** inhibitors)
IT Blood plasma
Blood serum
Blood
Signal transduction, biological
(retroviral transduction of cells using sol. **complement** inhibitors)
IT Therapeutics
(geno-, retroviral transduction of cells using sol. **complement** inhibitors)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, anti-**complement**; retroviral transduction of cells using sol. **complement** inhibitors)
IT Virus, animal
(retro-, retroviral transduction of cells using sol. **complement** inhibitors)
IT 80295-53-0, **Complement C5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitors; retroviral transduction of cells using sol. **complement** inhibitors)

L16 ANSWER 6 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:73261 HCAPLUS
DN 124:127101
TI Anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases
IN **Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven H.; Rollins, Scott**; Rother, Russell P.; Springhorn, Jeremy P.; Squinto,

Stephen P.; Thomas, Thomas C.; et al.
PA Alexion Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 159 pp.
CODEN: PIXXD2
PI WO 9529697 A1 951109
DS W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UG, US, UZ, VN
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
AI WO 95-US5688 950501
PRAI US 94-236208 940502
DT Patent
LA English
AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathol. conditions assocd. with GN. Also disclosed are novel anti-C5 antibodies and anti-C5 antibody-encoding nucleic acid mols. These antibodies are useful in the treatment of GN and other inflammatory conditions involving pathol. activation of the complement system.
IC ICM A61K038-36
ICS A61K039-00; A61K039-395; C07K014-00; C07K014-75; C07K016-00; C07K016-18; C07K016-36; C07K016-46; C12N005-10; C12N005-20; C12N015-09; C12N015-10; C12N015-13; C12N015-63; C12P021-02; C12P021-08
CC 63-3 (Pharmaceuticals)
Section cross-reference(s): 3, 15
ST antibody **complement C5** cloning glomerulonephritis sequence
IT Antigens
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(KSSKC epitope, antibodies binding to; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Hybridoma
Molecular cloning
Packaging materials
Polymerase chain reaction
Protein sequences
(anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Immune complexes
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(deposition of; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Immunoglobulins
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(G, anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Deoxyribonucleic acid sequences
(complementary, anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

IT Kidney, disease
(glomerulonephritis, anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Proteins, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(metabolic disorders, proteinuria, inhibition of; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(monoclonal, anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 173016-57-4
RL: NUU (Nonbiological use, unclassified); PRP (Properties); USES (Uses)
(PCR primer UDEC395; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 173016-56-3
RL: NUU (Nonbiological use, unclassified); PRP (Properties); USES (Uses)
(PCR primer UDEC690; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 172893-24-2P 173011-96-6P 173012-10-7P 173012-12-9P 173012-14-1P 173012-17-4P 173012-19-6P 173012-21-0P 173012-23-2P 173012-25-4P 173012-27-6P 173012-29-8P
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 173012-07-2, **Complement C5**, prepro- (human)
RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 80295-53-0, **Complement c5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(antibodies to; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 172998-82-2P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(epitope KSSKC-contg. antigen; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT 173012-09-4P 173012-11-8P 173012-13-0P 173012-15-2P 173012-16-3P 173012-18-5P 173012-20-9P 173012-22-1P 173012-24-3P 173012-26-5P 173012-28-7P 173012-30-1P

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(nucleic acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

IT 173146-43-5, Deoxyribonucleic acid (plasmid Apex-1) 173146-44-6, Deoxyribonucleic acid (plasmid Apex-3P) 173146-45-7
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleic acid sequence; anti-**complement C5** antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

L16 ANSWER 7 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:54415 HCAPLUS
DN 124:114995
TI In vitro and in vivo inhibition of **complement** activity by a single-chain Fv fragment recognizing human **C5**
AU **Evans, Mark J.**; **Rollins, Scott A.**; Wolff, Dennis W.; Rother, Russell P.; Norin, Allen J.; Therrien, Denise M.; Grijalva, Galo A.; Mueller, John P.; **Nye, Steven H.**; et al.
CS Dep. of Mol. Development, Alexion Pharmaceuticals, New Haven, CT, 06511, USA
SO Mol. Immunol. (1995), 32(16), 1183-95
CODEN: MOIMD5; ISSN: 0161-5890
DT Journal
LA English
AB Complement activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal antibody (N19-8) that recognizes the human complement protein C5 has been shown to effectively block the cleavage of C5 into C5a and C5b, thereby blocking terminal complement activation. In this study, a recombinant N19-8 scFv antibody fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human C5 and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit complement-mediated tissue damage, complement-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer contg. 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approx. 10 min after the addn. of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 h following the addn. of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma contg. the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 h. Pharmacokinetic anal. of N19-8 scFv serum levels

suggested a two-compartment model with a T1/2.alpha. of 27 min. These data suggest that recombinant N19-8 scFv is a potent inhibitor of the terminal complement cascade and may have potential in vivo applications where short duration inhibition of terminal complement activity is desirable.

CC 15-4 (Immunochemistry)

ST **complement C5** inhibition Ig Fv fragment; single chain Ig **complement C5** inhibition

IT Deoxyribonucleic acid sequences
Mouse
Protein sequences
(**complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)

IT **Complement**
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(**complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)

IT Immunoglobulins
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
(single-chain Fv fragment; **complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)

IT 172893-24-2
RL: PRP (Properties)
(amino acid sequence; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)

IT 80295-53-0, **Complement c5**
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(**complement** activity inhibition by single-chain Fv fragment recognizing human **C5**)

IT 82986-89-8, **Complement** c5b-9
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(hemolysis; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)

IT 166845-08-5, Genbank L43067
RL: PRP (Properties)
(nucleotide sequence; **complement** activity inhibition by a single-chain Fv fragment recognizing human **C5**)

L16 ANSWER 8 OF 12 HCAPLUS COPYRIGHT 1997 ACS

AN 1996:49519 HCAPLUS

DN 124:143157

TI Monoclonal antibodies directed against human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs

AU **Rollins, Scott A.**; **Matis, Louis A.**; Springhorn, Jeremy P.; Setter, Eva; Wolff, Dennis W.

CS Department of Immunobiology, Alexion Pharmaceuticals, Inc., New haven, CT, 06511, USA

SO Transplantation (1995), 60(11), 1284-92
CODEN: TRPLAU; ISSN: 0041-1337

DT Journal

LA English

AB The hyperacute rejection (HAR) of xenotransplanted organs is initiated by the deposition of natural antibodies on donor

endothelium followed by the activation of the recipient complement system, which rapidly destroys the graft. Studies of the role of activated complement in HAR have suggested that natural antibody as well as early (C3a, C3b) and the late (C5a, C5b-9) activated complement components may contribute to cell activation and damage. Attenuation of HAR has been achieved by blockade of C3 activation with sol. CR1 or consumptive depletion of complement with cobra venom factor; however, similar studies using specific inhibitors of terminal complement components have not been described. To address the contribution of C5a and the membrane attack complex (C5b-9, mAC) to complement-mediated xenogeneic cell and organ damage, we utilized functionally blocking monoclonal antibodies direct against the human terminal complements components C5 and C8. Our data show that both anti-C5 and anti-C8 mAbs protect porcine aortic endothelial cells from membrane damage mediated by human C5b-9. Addnl., both the anti-C5 and anti-C8 mAbs blocked complement-mediated generation of membrane prothrombinase activity on porcine aortic endothelial cells challenged with human serum. To test the ability of these antibodies to attenuate antibody and complement-mediated damage of xenogeneic organs, an ex vivo model was developed wherein isolated rat hearts were perfused with human serum in the presence or absence of the anti-C5 and anti-C8 mAbs. Our data demonstrate that mAbs directed against human C5 and C8 prevented organ damage by human serum complement and suggest that these mols. may serve as potent inhibitors of HAR.

CC 15-4 (Immunochemistry)

ST monoclonal antibody **complement C5** C8

IT Cytolysis
(monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs)

IT **Complement**
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs)

IT Blood vessel, disease
(endothelium, injury, monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs)

IT Heart, disease
(injury, monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs)

IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
(monoclonal, monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs)

IT Transplant and Transplantation
(xeno-, monoclonal antibodies to human **C5** and C8 block **complement**-mediated damage of xenogeneic cells and organs in relation to)

IT 80295-53-0, **Complement c5** 80295-58-5, **Complement** c8
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(monoclonal antibodies to human **C5** and C8 block

complement-mediated damage of xenogeneic cells and organs)

IT 80295-54-1, **Complement** C5a
RL: BSU (Biological study, unclassified); BIOL (Biological study) (role of C5a in **complement**-mediated damage of xenogeneic cells and organs)

IT 82986-89-8, **Complement** C5b-9
RL: BSU (Biological study, unclassified); BIOL (Biological study) (role of C5b-9 in **complement**-mediated damage of xenogeneic cells and organs)

L16 ANSWER 9 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1996:49512 HCAPLUS
DN 124:143156
TI **Complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation
AU Kroshus, Timothy J.; **Rollins, Scott A.**; Dalmasso, Agustin P.; Elliott, Eileen A.; **Matis, Louis A.**; Squinto, Stephen P.; Bolman, R. Morton, III
CS Department of Surgery, University of Minnesota, Minneapolis, MN, USA
SO Transplantation (1995), 60(11), 1194-202
CODEN: TRPLAU; ISSN: 0041-1337
DT Journal
LA English
AB Prevention of hyperacute xenograft rejection in the pig-to-primate combination has been accomplished by removal of natural antibodies, complement depletion with cobra venom factor, or prevention of C3 activation with the sol. complement inhibitor sCR1. Although these strategies effectively prevent hyperacute rejection, they do not address the relative contribution of early (C3a, C3b) vs. late (C5a, C5b-9) activated complement components to xenogeneic organ damage. To better understand the role of the terminal complement components (C5a, C5b-9) in hyperacute rejection, an anti-human C5 mAb was developed and tested in an ex vivo model of cardiac xenograft rejection. In vitro studies demonstrated that the anti-C5 mAb effectively blocked C5 cleavage in a dose-dependent manner that resulted in complete inhibition of both C5a and C5b-9 generation. Addn. of anti-C5 mAb to human blood used to perfuse a porcine heart prolonged normal sinus cardiac rhythm from a mean time of 25.2 min in hearts perfused with unmodified blood to 79, 296, or >360 min when anti-C5 mAb was added to the blood at 50 .mu.g/mL, 100 .mu.g/mL, or 200 .mu.g/mL, resp. In these expts., activation of the classical complement pathway was completely inhibited. Hearts perfused with blood contg. the highest concn. of anti-C5 mAb had no histol. evidence of hyperacute rejection and no deposition of C5b-9. These expts. suggest that the activated terminal complement components C5a and C5b-9, but not C3a or C3b, play a major role in tissue damage in the porcine-to-human model of hyperacute rejection. They also suggested that targeted inhibition of terminal complement activation by anti-C5 mAbs may be useful in clin. xenotransplantation.
CC 15-4 (Immunochemistry)
ST cardiac xenotransplant **complement** monoclonal antibody
IT Swine
(**complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)
IT **Complement**

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
(monoclonal, **complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT Transplant and Transplantation
(xeno-, **complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT Heart
(xenotransplant, **complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT 80295-54-1, **Complement** C5a
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**complement** inhibition with an anti-**C5** monoclonal antibody prevents acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

IT 82986-89-8, **Complement** C5b-9
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of **complement** C5b-9 in acute cardiac tissue injury in an ex vivo model of pig-to-human xenotransplantation)

L16 ANSWER 10 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1995:931533 HCAPLUS
DN 123:337462
TI Method for reducing immune and hemostatic dysfunctions during extracorporeal circulation
IN **Rollins, Scott A.**; Smith, Brian R.; Squinto, Stephen P.
PA Alexion Pharmaceuticals, Inc., USA; Yale University
SO PCT Int. Appl., 34 pp.
CODEN: PIXXD2
PI WO 9525540 A1 950928
DS W: AU, CA, JP
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AI WO 95-US3614 950322
PRAI US 94-217391 940323
DT Patent
LA English
AB The use of anti-C5 antibodies to reduce the dysfunction of the immune and hemostatic systems assocd. with extracorporeal circulation procedures, such as, cardiopulmonary bypass procedures, is disclosed. The antibodies have been found to significantly reduce complement activation, platelet activation, leukocyte activation, and platelet-leukocyte adhesion assocd. with such procedures. Demonstrated were anti-C5 monoclonal antibody inhibition of complement activity, generation of C3a, prevention of the generation of c5b-9, platelet and leukocyte activation and adhesion during extracorporeal circulation.
IC ICM A61K039-00
ICS A61K039-395; C07K016-00; C07K016-18
CC 15-3 (Immunochemistry)
ST monoclonal antibody **complement C5** extracorporeal circulation

IT Circulation
(extracorporeal, monoclonal anti-**C5** antibody for reducing immune and hemostatic dysfunctions during extracorporeal circulation)
IT Circulation
(extracorporeal, cardiopulmonary bypass, monoclonal anti-**C5** antibody for reducing immune and hemostatic dysfunctions during extracorporeal circulation)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, monoclonal anti-**C5** antibody for reducing immune and hemostatic dysfunctions during extracorporeal circulation)
IT 80295-43-8, **Complement** C3b
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(monoclonal anti-**C5** antibody for reducing immune and hemostatic dysfunctions during extracorporeal circulation)
IT 80295-53-0, **Complement C5** 80295-54-1, **Complement** C5a 80295-55-2, **Complement** C5b
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(monoclonal anti-**C5** antibody for reducing immune and hemostatic dysfunctions during extracorporeal circulation)

L16 ANSWER 11 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1995:805952 HCAPLUS
DN 123:196481
TI Anti-**C5** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease
AU Wang, Yi; **Rollins, Scott A.**; Madri, Joseph A.; **Matis, Louis A.**
CS Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT, 06511, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1995), 92(19), 8955-9
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Activated components of the complement system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target complement activation in immune-mediated joint inflammation, the authors have utilized monoclonal antibodies (mAbs) that inhibit the complement cascade at C5, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, the authors demonstrate the efficacy of a mAb specific for murine C5 in the treatment of collagen-induced arthritis, an animal model for RA. The authors show that systemic administration of the anti-C5 mAb effectively inhibits terminal complement activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-C5 mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a crit. role for activated terminal complement components not only in the induction but also in the progression of collagen-induced arthritis and suggest that C5 may be an attractive therapeutic target in RA.
CC 15-8 (Immunochemistry)
ST arthritis **C5 complement** monoclonal antibody

IT Arthritis
(anti-**C5 complement** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease)
IT Antibodies
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, anti-**C5 complement** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease)
IT Arthritis
(rheumatoid, anti-**C5 complement** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease)
IT Collagens, biological studies
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(type II, anti-**C5 complement** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease)
IT 80295-53-0, **Complement c5**
RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(anti-**C5 complement** monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease)

L16 ANSWER 12 OF 12 HCAPLUS COPYRIGHT 1997 ACS
AN 1995:727042 HCAPLUS
DN 123:141260
TI Rapid expression of an anti-human **C5** chimeric Fab utilizing a vector that replicates in COS and 293 cells
AU **Evans, Mark J.**; Hartman, Sandra L.; Wolff, Dennis W.; **Rollins, Scott A.**; Squinto, Stephen P.
CS Department of Molecular Development, Alexion Pharmaceuticals, Inc., 25 Science Park, New Haven, USA
SO J. Immunol. Methods (1995), 184(1), 123-38
CODEN: JIMMBG; ISSN: 0022-1759
DT Journal
LA English
AB Inhibition of complement system activation requires the development of sol. nonimmunogenic inhibitors with good tissue penetrating abilities that are themselves unable to activate complement. Chimeric mouse/human Fabs capable of blocking the activity of complement proteins are likely to fulfill these criteria. Several monoclonal antibodies that inhibit the activation of the human complement system have recently been developed. To examine the properties of chimeric Fab derived from these monoclonal antibodies, we have developed an expression system which allows the rapid prodn. of milligram quantities of chimeric Fab. Both the chimeric light chain and the chimeric Fd were co-expressed from the same vector, pAPEX-3P. This vector contains the SV40 origin of replication, which allows the rapid prodn. of chimeric Fab in COS cells for preliminary characterization. Addnl., pAPEX-3P contains the Epstein-Barr virus origin of replication and a puromycin selectable marker for maintenance as a stable episome in human cell lines. A prodn. system consisting of transfected 293-EBNA cells cultured in serum free medium followed by protein G-Sepharose chromatog. of the

conditioned medium was found to be sufficient for the rapid prodn. of purified chimeric Fab. Here we have utilized this expression system to demonstrate that an anti-human C5 chimeric Fab was a potent inhibitor of complement activation in both in vitro activation assays and an ex vivo model of complement-mediated tissue damage.

CC 15-3 (Immunochemistry)

ST pAPEX3P vector antibody Fab **C5 complement**

IT Genetic vectors
(pAPEX-3P; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)

IT Injury
(tissue; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)

IT Animal cell line
(293, rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)

IT Animal cell line
(COS, rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)

IT Antibodies
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(monoclonal, Fab; rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)

IT 80295-53-0, **Complement C5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(rapid expression of anti-human **C5** chimeric Fab by pAPEX-3P vector in COS and 293 cells and ex vivo model of **complement**-mediated tissue damage)